	Copyright		GenCore (c) 1993	Core 1993	version - 2003	5.1.6 Compugen Ltd.					* * * * * * *
OM nucleic - pro	protein search,		usir	ıg £	using frame_plus_	plus_n2p model					0.01
מס מחצ	October 1	16, 2	2003,		17:06:33 ; S (w) 141	Search time 8.77076 (without alignments)		Seconds updates/sec			
Title: Perfect score: Sequence:	US-09-673-274B-2_COPY_1_267 1 gataagcttatcggttcctg	1-274 sttat	B-2. cggt	G C	oY_1_132 stg	i tgaactgctggtgcgagact	gogagaet	: 132			மைப்ப
Scoring table:	BLOSUM62 Xgapop 10.0 Ygapop 10.0 Fgapop 6.0 Delop 6.0	0000		Xgapext Ygapext Fgapext Delext	. tt tt					3.8 4.8 8.8 9.8 9.8 9.8 9.8 9.8 9.8 9.8 9.8 9	மைமைமைம்
Searched:	127863 86	seds,	47026705	2670	35 residues						חוחו
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Command line parameters: -MODEL=frame+ n2p.model - DEV=xlp -0=/cgn2_1/USPTO_spool/US09673274/runat_16102003_170627_2531/app_query.fasta_1.6=/cgn2_1/USPTO_spool/US09673274/runat_16102003_170627_2531/app_query.fasta_1.6=/cspseprot_410FMT=fastanSUFFIX=rspMINMATCH=6.1LCOPELGLCOPEXT=0UNITS=bits_5TART=1END=-1MATRIX=blosum62TRANS=human40.cdiLIST=45DOCALIGN=200THR_SCORE=pctTHR_MX=100TRANS=human40.cdiLIST=45DOCALIGN=200THR_SCORE=pctTHR_MX=100TRANS=human40.cdiLIST=45DOCALIGN=200THR_SCORE=pctTHR_MX=100TRANS=human40.cdiLIST=45DOCALIGN=2000000000THR_SCORE=pct	rameters: 2p.model 0 spool/U 1-0FMT=f. ART=1 -ENI THR SCORE: RM=EXT -HI VITER -HI VITE	-DEV= 50967 30967 0=-1 -pct 2APSI	xlp 327 -Si -MA: -THI 2E=:	4/ru UFFI TRIX 500	unat_161020 IX=rsp -MIN (*blosum62 AX=100 -TH -MINLEN=0	03 170627_2531, MATCH=C.1LOOR - TRANS-humand - MIN-0 - ALIGN=: - MAXLEN=2000000	/app_que PCL=0 -1 .cdi -L1 15 -MODE 2000	ery.fasta_1.654 LCOPEXT=0 1ST=45 E=LOCAL	A H D D D O O O O O O O O O O O O O O O O	KESJLT I DEFN HELVI 10 DEFN HELVI AC P81544; DT 30 MAY-2000 DT 30-MAY-2000 DT 50-MAY-2000 DT DEFN HELVI AC P81544; AC P81	VI 0000 0003 0003 6 Vii
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Pred. No. score greater	io. is the number of restreater than or equal to derived by analysis of	umber or e	of qua sis	res of	sults predict the score the total	No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed a derived by analysis of the total score distribution.	to have being p	e a printed,	R R R R	ISSUE=Hemoly MEDLINE=99194 Lamberty M.,	emoly 9919
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Result No. Score			DB	ΙD		Dei	escription	ion	S S S S S S S S S S S S S S S S S S S	J. Biol. Chen	Cher
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ALIGNMENTS

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16 TCCTGCGTGTGGGGGGCTGTGACTACACTTCCGATTGCAACGGTGAGTGCAAGAGGAGG 75
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28-FEB-2003 (Rel. 41, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01.3AN 1990 (Rel. 13, Created)
01.3AN 1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 14, Last annotation update)
Alpra-1, Re neurotoxin II (Born III) (Bom3).
Buttous occitanus mardochei (Moroccan scorpion).
Buttousday pata, Metazoa, Arthropoda, Chelicerata, Arachnida, Scorpiones;
N(B1.7ax1D=6869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE 67161829; PubMed=3104036; Vargas C., Martin M.-F., Rochat H.; "Characterization of six toxins from the venom of the Moroccan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09 673 2748 2 (COPY 1 132 (1-132) x SCX3 BUTOM (1-66)
US-09-673-2748-2_COPY_1_332 (1-132) x DEFN_HELVI (1-44)
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Indels:

Length: Matches: Conservative: Mismatches:

0.00337 84.50 55.26% 39.47% 31.65%

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

TISSUE=Venom gland;
Zhang J.-H., Hua Z.C., Zhu D.X.;
"Cloning of anti-neuroexcitation peptide II (ANEP) cDNA from Scorpion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00505; Knotl; 1. Troxin; Neurotoxin; Ionic channel inhibitor;
                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anti-neuroexcitation peptide II precursor (ANEPII).
Anti-neuroexcitation peptide II precursor (ANEPII).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones; Buthoidea; Buthidae; Mesobuthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Buthus martensii Karsch.";
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
SUBCELLULAR LOCATION: Secreted (By similarity).
The STREE SPECIFICITY: Expressed by the venom gland.
SIMILARIY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.
ALPHA-TOXIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
ANTI-NEUROEXCITATION PEPTIDE II
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
C045C7DACBS13AB CRC64;
465619/60
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HSSP, P01491; 1B3C.
InterPro; IPR003614; Knot1.
InterPro; IPR002061; Scorpion_toxinL.
Pfam; PF00537; toxin_3; 1.
ProDom; PD000908; Scorpion_toxinL; 1.
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56
63
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9224 MW;
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EMBL, AF242737, AAK28342.1; ...
HSSP, P0.1494, 2SN3.
InterPro, IPR003514, Knot.:
InterPro, IPR003504, Scorpion toxin.
Pfam; PF00537, toxin_3; 1.
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SMART; SM00505; Knot1;
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88
81
81
83
63
63
47
                                                                             SEQUENCE FROM N.A.
TISSUE=Venom gland;
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Best Local Similarity:
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ID SCXC_CENTL
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                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GAGTGCAAGAGGAGGTTACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABPLysTyrThrGlyCysLygValTrpCysVallleAsnAsnGluSer---CysAsnSer 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GlucysLysIleArgGlyGlyTyrTyrGlyTyrCys---TyrPheTrpLysLeuAlaCys 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATAAGCTTATCGGTTCCTGCGTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGT 60
                                                                                                  28-FEB-2003 (Rel. 41, Last annotation update)
Neurotoxin AS precursor.
Mesobuthus martensii (Manchurian scorpion) (Buthus martensii).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Mesobuthus.
NCBI_TaxID=34649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09BKJ0: 09GZC4;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anti-neuroexcitation peptide III precursor (ANEPIII) (Anti-epilepsy
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEUROTOXIN AS.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
41286F9DDCC4FE90 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               882
127
227
227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JS-09-673-274B-2_COPY_1_132 (1-132) x SCAS_MESMA (1-85)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [ndels:
                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00537; toxin_3; 1.
Probom; PD000908; Scorpion_toxinL; 1.
SMART; SM00505; Knotl; 1.
SMART; Neurotoxin; Signal.
$1GNAL
                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003614; Knot1.
InterPro; IPR002061; Scorpion_toxin1.
                                                                                                                                                                                                                                                                                                                                            EMBL; AF079060; AAD47374.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81
56
63
65
9759 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.00
55.81%
44.19%
31.46%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 TGCTGCGAG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PheCysGln 66
                                                                                                                                                                                                                                                                                                                                                       HSSP; P01492; 1VNB
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                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity:
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Score:

SCN3 MESMA RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

TISSUE-Venom gland;
Zhang J.-H., Hua Z.C., Zhu D.X.;
"Cloning of anti-neuroexcitation peptide III (ANEP) cDNA from Scorprom
Buthus martensii Karsch.";
Submitted (MAR-2006) to the EMEL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCTGCGTGTGGGTGCTGTGAACTACACTTCCGATTGCAACGGTGAGTGCAAGAGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhang J.-H., Hua Z.C., Zhu D.X.,
"Cloning of anti-epilepsy peptide cDNA from scorpion Buthus martensii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Poxin, Neurotoxin, Ionic channel inhibitor, Sodium channel inhibitor,
peptide).
Mesobuthus martensii (Manchizian scorpion) (Buthus martensii).
Eukaryota: Metazoa, Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Mesobuthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 GGTTACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGCGAG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --- FUNCTION: Binds to sodium chancels and inhibits them.
--- SUBCELLUAR LOCATION: Secreted (By similarity).
---- TISSUE SPECIFICITY: Expressed by the venom gland.
---- SIMILARITY: BELOAUSS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.
ALPHA-TOXIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SlyAlaTyrTyrGlyTyrCysTrpThrTrp---GlyLeuAlaCysTrpCysGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCTENTIAL.
ANTI-NEURCEXCITATION PEPTIDE :1
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
K > 1 (IN REF. 2).
CIDGC93A2F82F8C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                Submitted (JAN-1999) to the BMFL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85
16
12
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CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 CysPheTrpLeuGlyLysAsn----GluAsnCysAspLysGluCysLysAlaLysAsn 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 TACAAGGGT-----GGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGCGAG 129
                                                                                                                                                                                                                                                                                                                                                              inplices Karsch.";
Bicchemistry 33:1135-11149(1994).
Finchemistry 33:1135-11149(1994).
Finchemistry 33:1135-11149(1994).
Finchick and the state of the state of the control of the activated channels, thereby blocking neuronal transmission.
FINCHELULAR LOCATION: Secreted.
FINSUS SPECIFICITY: Expressed by the venom gland.
FINITY: BELONGS TO THE ALEMANSETA-SCORPION TOXIN FAMILY.
BELOAT TOXIN SUBFAMILY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP: F01492; JVB8.
HSSP: F01492; JVB8.
InferPro; JPR001614; Knot1.
InferPro; JPR001614; Knot1.
InferPro; JPR001614; Soorpion_towind.
Property: Processes, Towing: J.
PRINTS; PR00208; Scorpion_towind.
Processes; Encorate; Jr.
SWART; SW00508; Scorpion_towind; J.
SWART; SW00505; Knot1; J.
JOKIN: MUTOCOMIN; John Channel Juhibitor; Sodium channel inhibitor.
JUSTIFIED 12 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDINE-95244424, PubMed=7727365, Lebreton F., Delepterre M., Ramitez A.N., Balderas C., Possani L.D., "Frimary and NNR three-dimensional structure determination of a novel crustacean toxin from the venow of the scorpton Centinioldes limpidus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-PEB-2003 (Rel. 41, Last annotation update)
Neurotoxin XIV precursor (Botl4).
Buthus occitanus tunetanus (Common European scorpion).
Bukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Scorpiones;
Butholdea, Buthidae, Buthus.
                                                                                                     Centruroldes limpidus limpidus (Mexican scorpion).
Eukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Scorpiones;
Buthoidea, Buthidae, Centruroldes.
NCBI TaxID=29941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 AA; 7338 MW; A478E63796F54DAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JS-09-673-2748-2_COPY_1_132 (1-132) x SCXC_CENLL (1-66)
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Matches:
Conservative:
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Indels:
  P45667,
01 NCV-1995 [Rel. 32, Created]
1-NCV-1995 (Rel. 32, Last sequence update)
28 FEB-2003 (Rel. 41, Last annotation update)
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                                                                                       Crustacean-specific toxin l.
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79.50
53.85%
43.59%
29.78%
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TISSUE-Veriom;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=6871;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | SCXE BUTOC
| Q17254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01330.813
01330.813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 GGTTACAAGGGTGGTCACTGCGGT----TCCTTCGCTAACGTGAACTGCTGCTGCTGGGG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 TCCTGCGTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGTGAGTGCAAGAGAGGAGG 75
                                                                                                                                                                Lor. J. Biochem. 218:653-660(1996).

-!- FUNCTION: Binds to sodium channels and inhibits the inactivation of the activated channels; thereby blocking neuronal transmission. This toxin is active only on insects.

-!- SUBCELLUAR IOCATION: Secreted.

-!- TISSUE SPECIFICITY: Expressed by the venom gland.

-!- SIMILARITY: BELCNGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.

ALPHA-TOXIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProDom; PD003908; ScErpton toxinL; 1.
SMART; SM0565; Knotl; 1.
Toxin; Neurotoxin; Ionic channel inhibitor; Sodium channel inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
18-SEP-2003 (Rel. 42, Last annotation update)
18-SEP-2003 (Rel. 42, Last annotation update)
18-SEP-2003 (Rel. 40, Last monotation update)
Buthus occitanus mardochei (Moroccan scorpion).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Buthus.

[1]
                                                                     Karoui H.; "A recombinant insect-specific alpha-toxin of Buthus occitanus
                                                                                                                         tunetanus scorpion confers protection against homologous mamma
MEDLINE=96300228; PubMed=8706664;
Bouhaouala-Zahar B., Ducancel F., Zenouaki I., Ben Khalifa R.
Borchanı L., Pelhate M., Boulain J.C., el Ayeb M., Menez A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
4977F16C511F0567 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-673-274B-2_COPY_1_132 (1-132) x SCXE_BUTOC (1-85)
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Mismatches:
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NEUROTOXIN XIV.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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PIR, S68906; S68956.
HSSP, P56678; IBMR.
InterPro; IPR002641; Knotl.
InterPro; IPR002661; Scorpion_toxinL.
Pfam; PF00537; toxin_3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9174 MW;
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50.00%
35.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1199
300
34
441
7 AA;
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Best Local Similarity:
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DISULFID
DISULFID
SEQUENCE
                                                                                                                                                     toxins.";
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SIGNAL
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Percent Similarity:
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                                                                                                                                                                   Bur. J. Neurosci. 11:975-985(1999).

-!- FUNCTION: Binds to sodium channels and infibits the inactivation of the activated channels, thereby blocking newronal transmission.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom gland.
-!- MASS SPECIFICITY: WM-7287.96; MW-8FR-0.37; METHOD-Electrospray.
-!- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.
ALPHA_TOXIN SUBFAMILY. ALPHA-LIKE TOXIN SUBCLASS.
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MEDLINE-90037062; PubMed=2808423;
Bougis P.E., Rochat H., Smith L.A.;
"Precursors of Androctonus australis scorpion neurotoxins. Structures of precursors, processing outcomes, and expression of a functional
                                                             Cestele S., Stankiewicz M., Manauelle P., De Waard M., Dargent B., Gilles N., Pelhate M., Rochat H., Martin-Bauclaire M.-F., Gordon D., "Scorpion alpha-like toxins, toxic to both mammals and insects, differentially interact with receptor site 3 on voltage-gated sodium channels in mammals and insects."
                                                                                                                                                                                                                                                                                                                                                                                                                    Toxin; Neurotoxin; Ionic channel inhibitor; Sodium channel inhibitor
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Eukaryota: Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Androctonus.
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BEDIJINE-79148414, PubMed-428402;

KOPEYAN C., Martinez G., Rochat H.;
"Amino acid sequence of neurotoxin III of the scorpion Androctonus
SEQUENCE, PHARMACOLOGICAL CHARACTERIZATION, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4305EB32436A4B90 CRC64;
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Conservative:
Mismatches:
Indels:
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01-JUL-1993 (Rel. 26, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Neurotoxin III precursor (AaH III) (AaH3).
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ProDom; PD000908; Scorpion_toxinL; 1.
SMART; SM00505; Knot1; 1.
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                        TISSUE=Venom;
MEDLINE=99203324; PubMed=10103091;
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Best Local Similarity:
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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--- TISSUE SPECIFICITY: Expressed by the venom gland.
--- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.
ALPHA-TOXIN SUBFAMILY.
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Pro000n; PD000908; Socrption_toxinL; 1.
SMART; SM03505; Knocl; 1.
Toxin; Neurotoxin; Jonic channel inhibitor; Sodium channel inhibitor;
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                                                                                                                                              STRUCTURE BY NMR.
MEDLINE=91122921; PubMed=2279844;
Laplante S.r., Mikov A., Robin M., Guittet E., Delsuc M.A.,
Charpentier I., Lallemand J.-Y.;
"Rapid determination and NMR assignments of antiparallel sheets and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRUCTURE BY NMR.

MIROLINE=93044377; PubMed=1422146;

Mikou A., Laplante S.R., Guittet E., Lallemand J.-Y.,

Martin-Eauclaire M.-F., Rochat H.;

"Toxin III of the scorpion Androctonus australis hector: proton

"Toxin III of the scorpion Androctonus australis hector: proton

"Toxin III of the scorpion Androctonus australis hector: proton

"Toxin III of the scorpion Androctonus australis hector: proton

"Toxin III of the scorpion Androctonus augustalis hector: ";

"Toxin III of the scorpion Androctonus augustalis the inactivation."

"In Proceedings of the State of State of the State o
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                              helices of a scorpion and a cobra toxin.",
Int. J. Pept. Protein Res. 36:227-230(1990)
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austrialis Hector.";
Eur. J. Biochem. 94:609-615(1979).
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Aliqnment Scores:
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                                                                                                                                                                                                                                                                                               Hamon A., Gilles N., Sautiere P., Martinage A., Kopeyan C., Jlens C., Tytgat J., Lancelin J.-M., Gordon D.; Tytgat J., Lancelin J.-M., Gordon D.; Characterization of scorpion alpha-like toxin group using two new texts from the scorpion Leuruns quinquestriatus hebraeus."; Eur. J. Blochem. 269:3920-3933(2002).

FUNCTION Bands to sodium channels and inhibits the inactivation of the activated channels, thereby blocking neuronal transmission. This toxin is highly toxic to insects and mice, and inhibits the birding of alpha-toxin to cockroach neuronal membranes.

SubCELLULATY: Expressed by the venom gland.

FISSUE SPECIFICITY: Expressed by the venom gland.

FISSUE SPECIFICITY: Expressed by the venom gland.

FISSUE SPECIFICITY: Expressed by the venom gland.
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P01489;
21-JUL-1986 (Rel. 01, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Meurotoxin IV (Lgq IV) (Lgq4).
Leiurus quinquestriatus quinquestriatus (Egyptian scorpion).
Eukaryota; Metazoa; Arthopoda; Chelicerata; Arachnida; Scorpiones; Butholdea; Buthadae; Leiurus.
SCL6_LEICH STANDARD; PRT; 64 AA.
P59156;
28 FEB 2003 (Rel. 41, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Alpha like neurocoxin Lqh VI (Lqh6;
Leivius quinquestriatus hebraeus (Yellow scorpion).
Leivius quinquestriatus hebraeus (Yellow scorpion).
Butholdea; Buthidae; Leiurus.
NCBI_Tax10=6884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               germanica).
1. SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.
ALPHA-TOXIN SUBFAMILY. ALPHA-LIKE TOXIN SUBCLASS.
                                                                                                                                                                                                                                     SEQUENCE, PHARMACOLOGICAL CHARACTERIZATION, AND BIOASSAY
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AMIDATION.
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam, PF60537, toxin_3, 1.
ProBom, PD660908, Scorpion_toxinL, 1.
                                                                                                                                                                                                                                                             TISSUE:Veloom;
MEDLINE=22168983; Pubmed=12180969;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
34
44
46
64
63 MW;
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77.50
51.28$
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16
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24
64
64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
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SEQÜENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cuery Match:
58:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCX4_LEIQU
ID SCX4_L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPETER SECOND TO COURT WERE WAS BEEN OF COURT OF
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70 AGGAGGGTTACAAGGGTGGTCACTGC------GGTTCCTTCGCTAACGTGAACTGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 AsnCysValTyrThrCysGlySerAsnSerTyr-----CygAsnThrGluCysThr 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::: ||| ::: |||| |||| 29 LysAsnGlyAlaGluSerGlyTyrCysGlnTrpLeuGlyLysTyrGlyAsnAla---Cys 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 TCCTGCGTGTGG-----GGTGCTGTGAACTACACTTCCGATTGCAACGGTGAGTGCAAG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00284; TCXĪN.
Probom, PD000989; Scorption_toxinL; 1.
SWART; SM0505; Knotl; 1.
Toxin; Neurotoxin; Ionic channel inhibitor; Sodium channel inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neurotoxin AS-1 precugsor
Resobuthus martensii (Manchurian scorpion) (Buthus martensii).
Bukaryota; Metazoa; Arfarofpda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Mesobuthus.
                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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AMIDATION.
882102ECIC2B89F6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Lasť sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps:
                                                                                                                                                                              InterPro; IPR003614; Knotl.
InterPro; IPR001219; Newcotoxin.
InterPro; IPR002061; Scorpion_toxinL.
Pfam; PF00537; toxin_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                     64
37
47
49
65
7202 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     77.50
57.14%
38.10%
29.03%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                   PIR; A01749; NTSR4L.
HSSP; P45697; 1SN1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 TGGTGC 126
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17
23
27
65
65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=34649;
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                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGTCCAAGAGGGGGTTACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                           GATAAGCTTATCGGTTCCTGCGTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |||||||||| ||| ::: ||| ||| 45 GluCysLyBLeuArgArgGlyAsnTyrGlyTyrCys---TyrPheTrpLySLeuAlaCys 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 AsnLysTyrThrGlyCysLysIleTrpCysVallleAsnAsnGluSer---CysAsnSer 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leiurus quinquestriatus quinquestriatus (Egyptian scorpion).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Leiurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Primary structure of scorpion anti-insect toxins isolated from the venom of Leiurus quinquestriatus quinquestriatus.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kopeyan C., Mansuelle P., Sampieri F., Brando T., Bahraoui E.M.,
Rochat H., Granier C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93160530; PubMed=8431601;
Zlotkin E., Gurevitz M., Fowler E., Adams M.E.;
"Depressant insect selective neurotoxins from scorpion venom:
                                                                                                                                                                                                                                 BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
E2274838439E2B95 CRC64;
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1.7
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                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                        NEUROTOXIN AS-1.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Insect toxin 2 (Insect toxin LqqIT2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AA
                                                                                                                                                                                                                                                                                                                                 Matches:
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                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                       InterPro; IPR003614; Knot1.
InterPro; IPR002061; Scorpion_toxinL.
Pfam. PF0057; toxin_3; 1.
SPCODOM; PD000908; Scorpion_toxinL; 1.
SMART; SM00505; Knot1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90184494; PubMed=2311768;
                                                                                                                  EMBL; AF079061; AAD47375.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FBS Lett. 261:423-426(1990)
                                                                                                                                                                                                                                                                                   9802 MW;
                                                                                                                                                                                                                                                                                                                                77.00
53.49%
39.53%
28.84%
ALPHA-TOXIN SUBFAMILY
                                                                                                                                                                                               Toxin; Neurotoxin; Signal SIGNAL 1 19
                                                                                                                                                                                                                                                                                                                     0.0327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 TGGTGCGAG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :::||||||
64 TyrCysGlu 66
                                                                                                                              P01492; 1VNB
                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
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ID SIX2_LEIQU
AC P19855;
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DISULFID
DISULFID
SEQUENCE
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                                                                                                                                                                  -!- FUNCTION: Binds to sodium channels and inhibits the inactivation of the activated channels, thereby blocking neuronal transmission. This toxin induces a slow, depressant, flaccid paralysis on fly larvae. It is active only on insects.
-!- SUBCELLULAR LOCATION: Secreted.
-!- ISUE SPECTICITY: Expressed by the venom gland.
-!- SIMILARITY: BELOWGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 SerCysLeuPheGly-----AsnGluGlyCysAsnLysGluCysLysSerTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Binds to sodium channels and inhibits the inactivation of the activated channels, thereby blocking neuronal transmission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Amino acid sequence of 2 neurotoxins from the scorpion Buthus eupeus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sodium channel inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Buthus eupeus (Lesser Asian scorpion) (Mesobuthus eupeus).
Eukaryota: Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Mesobuthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 GGTTACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGCGAG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GlyGlySerTyrGlyTyrCysTrpThrTrp---GlyLeuAlaCysTrpCysGlu 45
                                                                                                 Ziotkin E., Fowler E., Eitan M., Moyer M., Adams M.E.; "On the chemistry and action of the depressant insect toxins."; Toxicon 28:170-170(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-85046632; Pubmed-6497916;
Volkova T.M., Garsia A.F., Telezhinskaya I.N., Potapenko N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMAKH; SMUUDDOS; AUCLI, 4.

DISULFID 10 60 BY SIMILARITY.

DISULFID 14 35 BY SIMILARITY.

DISULFID 2: 42 BY SIMILARITY.

DISULFID 25 44 BY SIMILARITY.

SECURNCE 61 AA, 6860 MW, 80F01771C7DCFAF6 CRC64;
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SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: Expressed by the venom gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-673-274B-2_COPY_1_332 (1-132) x SIX2_LEIQU (1-61)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
chemistry, action, and gene cloning.";
Arch. Insect Biochem. Physiol. 22:55-73(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00537; toxin 3; Probom; PD000908; Scorpion toxinL; 1. SMART; SM00505; Knot1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                          HSSP, P01494, ZSN3.
InterPro, IPR003614, Knoti.
InterPro, IPR002061; Scorpion_texini.
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76.50
55.26%
39.47%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28.65
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                                                                                                                                                                                                                                                                                                                                                                                            PIR; B34123; B34123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
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                                                                              ACTION.
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DB:
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STRAND
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DB:
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                                                                                                                                                                                                                                                                                                                                 22 CysAspSerGluCysLysLysAsnGlyAlaAspGlySerTyrCysGlnTrpLeuGlyArg 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kilms I., Trivelli X., Lancelin J.-M.; "A cis trans isomerism of a non-proly! peptide bond in LOH III alpha-like scorpion toxin revealed by solution NMR.";
                      PIR, UT0020, NTSR4E.
HSSP, P45697, ISNI.
InterPro, IPR003614; Knotl.
InterPro, IPR003614; Scorpion_toxinL.
InterPro, IPR00219; Neurotoxin.
InterPro, IPR00219; Noxin_3; I.
PRIMTS, PR00537; toxin_3; I.
PRIMTS, PR005984; Toxin_3; I.
SMART; SM00508; Scorpion_toxinL; I.
SMART; SM00508; Knotl; I.
Toxin; Neurotoxin; Ignic channel inhibitor; Scotium channel inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Leiurus guinquestriatus hebraeus (Yellow scorpion).
Eukaryota; Merazoa; Atthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Leiurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gordon D., Lancelin J.-M.;
Wilk structures and activity of a movel alpha-like toxin from the
scorption Leiurus quinquestriatus hebraeus.";
J. Mol. Biol. 285:1749-1763(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "New toxins acting on sodium channels from the scorpion Leiurus quinquestitatus hebraeus suggest a clue to mammaliam vs insect
TO THE ALPHA/BETA-SCORPICN TOXIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Venom;
MEDLINE=88353091; PubMed=9690781;
Sautiere P., Cestele S., Kopeyan C., Martinage A., Drobecq H., Doljansky Y., Gordon D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-99141414, PubMed-9917409;
Krimm I., Gilles N., Sautiere P., Stankiewicz M., Pelhate M.,
Gordon D., Lancelin J.-M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE, PHARMACOLOGICAL CHARACTERIZATION, AND BICASSAY
                                                                                                                                        BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                           US-09-673-2748-2_COPY_1_32 (1-132) x SCXE_BUTEU (1-66)
                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 JUL 1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 42, Last annotation update)
Alpha-like neurotoxin Lqh III (Lqh3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 A.A.
                                                                                                                                                                                                                                                                          Inde:s:
                                                                                                                                                                                                                                                                                                                                                                               103 TTCGCTAACGTGAACTGCTGGTGCGAG 129
                                                                                                                                                                                                                                                                                                                                                                                           7453 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  selectivity.";
Toxicon 36:1141-1154(1998).
                                                                                                                                                                                                                          0.0435
76.00
58.62%
44.83%
 SIMILARITY: BELONGS TA
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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16
22
26
66 AA;
                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI TaxID=6884;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :SSUE=Venom;
                                                                                                                                                                                                                Alignment Scores:
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P56678;
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11 AsnCysValTytHisCysPheProGlySerSerGlyCysAspThrLeuCysLysGluLys 30
              --- FUNCTION: Binds to sodium channels and inhibits the inactivation of the activated channels, thereby blocking neuronal transmission. Active on both insects and mammais but competes for alpha-toxins binding only on cockroach sodium channels.
--- SUBDNIT: Monomer.
--- SUBCELLULAR LOCATION: Secreted.
---- TISSUE SPECIFICITY: Expressed by the venom gland.
---- MISCELLANBOUS: LD (50) is 50 mg/kg by intracerebroventricular injection into mice.
---- SIMILARITY: BELOWGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.
ALPHA-TOXIN SUBFAKILY. ALPHA-LIKE TOXIN SUBCLASS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 GGTTACAAGGGTGGTCACTGCGGTTCCTTCGCT-----AACGTGAACTGCTGGTGC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM05605; Knctl; I. Towns, Towns, Sodium channel inhibitor; Amidation; 3D-structure.
Amidation; 3D-structure.
65
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Matches:
Conservative:
Mismatches:
Submitted (JUL-2000) to the PDB data bank.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMIDATION
                                                                                                                                                                                                                                                                         PDB; 1EMR; 16-FEB-99.
PDB; 1FH3; 08-NOV-06.
InterPro; 1FR003614; Knctl.
InterPro; 1FR003614; Scorpion_tox:nl.
Pfam; PF00537; toxin 3; 1.
Profom; PD300908; Scorpion_toxinL; 1.
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Query
Match 1
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No.
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| SIDSI/gcgdata/geneseq_geneseqp_embl/AA1980.DAT:•
| SIDSI/gcgdata/geneseq_geneseqp_embl/AA1981.DAT:•
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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                    protein search, using frame_plus_n2p model
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Maximum Match 100%
Listing first 45 summaries
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267
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Ygapop 10.0,
Fgapop 6.0,
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Antifunga//antibac

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ABB76897 ABB76882

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ABB76876 ABB76877 ABB76881

Antifungal/antibac Antifungal/antibac Antifungal/antibac

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                                                                                                                                                                                                                                                                                                                                                                                                                                        Heliomycin; polycysteine peptide; antifungal; antibacterial; fungal infection; plant protection; animal protection; transgenic plant; budgi; bacteria; Cercospora belicola; Cladosporium herbarum; Fusarium culmorum; F. oxysporum;
                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of a heliomycin peptide
                                                                                                                                                                                                                                                                                                                                                 ALIGNMENTS
                                                                                                                                                                                                                              ABB76886
ABB76880
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AB376887
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ABB76878
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ABP55988
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                                                                                                                                                                                                                                                                                                                                                                               AAYS4375 standard; Peptide; 44
Phytophthora cinnamoni
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Alignment Scores:
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                                                                              Dimarcq J,
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                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                    Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents the heliomycin peptide. Heliomycin is a polycysteine peptide with antifungal and antibacterial activity, isolared from the leptide with antifungal and antibacterial activity. Contain the sequence given in AAY5478. The heliomycin peptides contain the sequence given in AAY5478. The heliomycin peptides are used as pharmaceuticals for treating or preventing fungal infections in himans and animals. They may also be used as antifungal agents for plant protection. Nucleic acid encoding the heliomycin peptides is used to generate transgenic plants that are resistant to some fungil and because the parterial specifically Cercespora beticola, Cladusporium herbarum, busature culmonum, F. oxysporium and Phytophinora cinnamonil, and for recombinant production of the peptides.
                                                                                                                               New polycysteine peptides, designated heliomycin, with antifungal or antibacterial activity, useful in medicine or plant protection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antifungal, antibacterial; fungicide; heliomicine; human medicine; veterinary medicine; plant protection; bacterial infection;
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4 4
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Matches:
Conservative:
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Indels:
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                                                                                                                                                               Claim 7; Page 31-32; 46pp; French.
                                                                                (RHCN ) RHONE POULENC AGROCHIMIE
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267.00
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                                                                                                   2000-108532/10.
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Query Match:
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                                                             15-APR 1998;
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                                         15 APR 1998;
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Pred. No.:
  FR2777568 AI
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61 GAGTGCAAGAGGGGTTACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGC 120
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                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to peptide derivatives of heliomicine with antifungal and/or antibacterial activity. The present sequence is one such peptide. The peptides are useful in human and veterinary medicine and in plant protection, for control of bacterial and fungal infections. An antifungal and/or antibacterial composition containing at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AspLysLeulleGlySerCysValTrpGlyAlaValAsnTyrThrSerAspCysAsnGly 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GATAAGCTTATGGGTTCCTGCGTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGT
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                                                                                                                                                                                                                                                                                New peptide derivatives of heliomicine, useful as antibacterial an
antifungal agents in human or veterinary medicine and agriculture
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Matches:
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                               Claim 15; Page 57; 100pp; French.
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19-SEP-2000; 2000FR-0011949.
                                              13-JUL-2000; 2000FR-0009248.
19-SEP-2000; 2000FR-0011949.
05-JUL-2001; 2001WO-FR02164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide is also claimed.
                                                                                                                                                                              Legrain M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 TrpCysGluThr
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Best Local Similarity:
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05-JUL-2001; 2001WO-FR02164.
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                                                                                                                                                                                                                                      The present invention relates to peptide derivatives of heliomicine with antifungal and/or antibacterial activity. The present sequence is one such peptide. The peptides are useful in human and veterinary medicine and in plant protection, for control of bacterial and fungal infections. An antifungal and/or antibacterial composition containing at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AspLysLeulleGlySerCysValTrpGlyAlaValAsnTyrThrSerAspCysAsnGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATAAGCTTATCGGTTCCTGCGTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGT
                                                                                                                                  New peptide derivatives of heliomicine, useful as antibacterial and antifungal agents in human or veterinary medicine and agriculture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "residues derived from the yeast Mat-alphal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid seguence of a fusion peptide of MF-alpha1/heliomycin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mat alphal factor, MF-alphal, heliomycin, polycysteine peptide, antifungal, antibacterial; fungal infection; plant protection; animal protection; transgenic plant, fungi; bacteria; Cercospora beticola; Cladosporium herbarum; Fusarium culmorum; F. oxysporum; Phytophthora cinnamoni.
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Conservative:
Mismatches:
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/note= "heliomycin residues"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY54374 standard; Peptide; 49 AA
                                                                                                                                                                                                   Claim 15; Page 57; 100pp; French.
                                              Menin L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98FR-0004933.
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                                                                                                                                                                                                                                                                                                                                                                peptide is also claimed
                                            Legrain M,
                                                                                        WPI; 2002-179779/23
(ENTO-) ENTOMED SA.
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                          44 AA;
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                                            Dimarcq J,
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derived from the Mat apparation (MF-alphal) and hellomyon. The attachment of the MF-alphal sequence to the N-terminal aids secretion of the Hellomycin is a polyoyteteine peptide with antifungal and antibacterial activity, isolated from the leplodopteron Hellothis virescens. Hellomycin peptides contain the sequence given in AAY54378. The hellomycin peptides are used as pharmaceuticals for iterating or preventing fungal infections in humans and animals. They may also be used as attifungal agents for plant protection. Nucleic acid encoding the hellomycin peptides is used to generate transgenic plants that are resistant to some fungi and bacteria (specifically F. oxysporum and Phytophthora cinnamoni), and for recombinant production of the peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 GluCysLysArgArgGlyTyrLysG.yGlyH.sCysGlySerPheAlaAsnValAsnCys 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GAGTGCAAGAGGAGGGTTACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGC
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                                                                                                                                                                      New polycysteine peptides, designated heliomycin, with antifungal antibacterial activity, useful in medicine or plant protection
                                                                                                                                                                                                                                                                                                       present sequence represents a fusion peptide of 5 amino acids
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                                            (RHON ) RHONE-POULENC AGROCHIMIE.
                                                                                                                                                                                                                                                  Claim 13; Page 31; 46pp; French
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                                                                                                 WPI; 2000-108532/10
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Best Local Similarity:
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15-APR-1998;
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The present invention relates to peptide derivatives of heliomicine with antifungal and/or antibacterial activity. The present sequence is one such peptide. The peptides are useful in human and verexinary medicine and in plant protection, for control of bacterial and fungal infections. An antifungal and/or antibacterial composition containing at least one peptide is also claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GATAAGCTTATCGGTTCCTGCGTGTCGGGTGCTGTGAACTACCCATTGCCAATTGCAACGGT
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                                                                                New peptide derivatives of heliomicine, useful as antibacterial and antifungal agents in human or veterinary medicine and agriculture
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Mismatches:
Indels:
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Matches:
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                                                                                                                                              Claim 15; Page 57; 100pp; French
  Menir L.
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                                                                                                                                                                                                                                                                                                      The present invention relates to peptide derivatives of heliomicine with antifurgal and/or antibacterial activity. The present sequence is one such peptide. The peptides are useful in human and vererinary medicine and in plant protection, for control of bacterial and fungal infections. An antifurgal and/or antibacterial composition containing at least one peptide is also claimed.
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                                                                                                                                                                                                             New peptide derivatives of heliomicine, useful as antibacterial and amplingal agents in human or veterinary medicine and agriculture
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19-SEP-2000; 2000FR-0011949.
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19 SEP 2000, 2000FR-0011949.
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19-SEP-2000, 2000FR-0011949.
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                      Claim 15; Page 57; 100pp; French.
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and in plant protection, for control of bacterial and fungal infections. An antifungal and/or antibacterial composition containing at least one peptide is also claimed.
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US-09-673-274B-2_COPY_1_132 (1-132) x ABB76862 (1-44)
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The present invention relates to peptide derivatives of heliomicine with antifungal and/or antibacterial activity. The present sequence is one such peptide. The peptides are useful in human and veterinary medicine and in plant protection, for control of bacterial and fungal infections. An antifungal and/or antibacterial composition containing at least one
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Best Local Similarity:
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                                                                                                                                                                                                                                                                   W0200206324 - A2
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                                                                                                                                  03-JUL-2002
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                                                                                                         ABB76869;
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DB:
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                       61 GAGTGCAAGAGGAGGGTTACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to peptide derivatives of heliomicine with antifungal and/or antibacterial activity. The present sequence is one such peptide. The peptides are useful in human and veterinary medicine and in plant protection, for control of bacterial and fungal infections. An antifungal and/or antibacterial composition containing at least one peptide is also claimed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 GluCysLysArgArgGlyTyrLysGlyGlyHisCysGlySerPhelleAsnValAsnCys 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AspLysLeuileGlySerCysValTrpGlyAlaValAsnTyrThrSerAspCysAsnGly 20
AspLysLeulleGlySerCysValTrpGlyAlaValAsnTyrThrArgAspCysAsnGly 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GATAAGCTTATCGGTTCCTGCGTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New peptide derivatives of heliomicine, useful as antibacterial and antifungal agents in human or veterinary medicine and agriculture
                                                                                                                                                                                                                                                                Antifungal; antibacterial; fungicide; heliomicine; human medicine; veterinary medicine; plant protection; bacterial infection;
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Mismatches:
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Matches:
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                                                                                                                                                                                                                                      Antifungal/antibacterial peptide pEM22
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                                                                                                                                                         ABB76867 standard; Protein; 44
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262.00
97.73%
97.73%
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19-SEP-2000; 2000FR-0011949.
                                                                                                                                                                                                              (first entry)
                                                                             TGGTGCGAGACT 132
                                                                                                   41 TrpCysGluThr 44
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est Local Similarity:
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                                                                                                                                                                                                                                                                                          fungal infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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The present invention relates to peptide derivatives of hellomicine with antifungal and/or antibacterial activity. The present sequence is one such peptide. The peptides are useful in human and vecerinary medicine and in plant protection, for control of bacterial and fungal infections. An antibungal and/or antibacterial composition containing at least one peptide is also claimed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New peptide derivatives of helichicine, useful as antibacterial and antifungal agents in human or veterinary medicine and agriculture
                                                                                                                                                                                             Antifungal, antibacterial, fungicide, heliomicine, human medicine, vererinary medicine, plant protection, bacterial infection, fungal infection.
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Mismatches:
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Matches:
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                                                                                                                                                       Antifungal/antibacterial peptide pEM25
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ABB76869 standard; Protein; 44
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The present sequence represents a fusion peptide of the tobacco PR-lalpha signal peptide and hellomycin. The attachment of the CPR-lalpha sequence to the N-terminal aids secretion of the heliomycin peptide. Hellomycin is a polytysteine peptide with antifungal and antibacterial activity, isolated from the lepidopteron Heliothis virescens. Heliomycin peptides contain the sequence given in AAY5478. The heliomycin peptides are used as pharmaceuticals for treating or preventing fungal infections in humans and animals. They may also be used as antifungal agents for plant protection. Nucleic acid encoding the heliomycin peptides is used to generate transgenic plants that are resistant to some fungi and bacteria (specifically Cercospora beticola, Cladosporium herbarum, Fusarium culmorum, production con the peptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 GAGTGCAAGAGGAGGGTTACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGC 120
                                PR-lalpha; heliomycin; polycysteine peptide; antifungal; antibacterial; fungal infection; plant protection; animal protection; transgenic plant; fungi; bacteria; Cercospora beticola; Cladosporium herbarum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GATAAGCTTATCGGTTCCTGCGTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polycysteine peptides, designated heliomycin, with antifungal or antibacterial activity, useful in medicine or plant protection \cdot
                                                                                                                                                                                                              /note= "tobacco PR-lalpha signal peptide"
A fusion peptide of PR-lalpha signal peptide/heliomycin.
                                                                                     Fusarium culmorum; F. oxysporum; Phytophthora cinnamoni
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                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                      /note= "heliomycin"
                                                                                                                                                                                                                                                                                                                                                                                                                                    (RHON ) RHONE-POULENC AGROCHIMIE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 13; Page 32; 46pp; French
                                                                                                                           Chimeric - Nicotiana sp.
Chimeric - Heliothis virescens.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                  15-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to peptide derivatives of heliomicine with antifungal and/or antibacterial activity. The present sequence is one such peptide. The peptides are useful in human and veterinary medicine and in plant protection, for control of bacterial and fungal infections. An antifungal and/or antibacterial composition containing at least one peptide is also claimed.
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                                                                                                                                              Antitungal, antibacterial, fungicide, heliomicine, human medicine, veterinary medicine, plant protection, bacterial infection,
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                                                                                                             Antifungal/antibacterial peptide pEM7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAYS4376 standard; Peptide; 74
     ABB76871 standard; Protein; 44
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262.00
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19 SEP-2000; 2000FR-0011949.
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Best Local Similarity:
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                                                                                                                                                                                       fungal infection.
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Heliothis virescens (Noctuid moth) (Owiet moth).
Eukaryota, Merazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endobterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
Noctuidae, Heliothinae; Heliothis.
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Mismatches:
Indels:
Gaps:
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30-MAY-2000 (Rel. 39, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
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Matches:
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SIX4_BUTOC
SIX5_BUTOC
SIX5_BUTOC
SIX5_CENSC
DEFIJ_CENSC
DEFIJ_CENSC
SICH_CENSC
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SIX4 BUTSI
SCX1 BUTCO
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SC17_MESMA
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                                                  SECUENCE, AND CHARACTERIZATION.
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PDB; 112U; 12-FEB-02
PDB; 112V; 12-FEB-02
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22
44 AA;
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Best Local Similarity:
Alignment Scores:
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ID DEFN HELVI
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P1348 buthus occi
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P45658 androctonue
P41964 drosophila
                                                                                                                  October 16, 2003, 17:06:33 ; Search time 11.2292 Seconds (without alignments) 1415.504 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                          1 gataagettateggtteetg.....gaaegtgtegaeggateegg 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                 - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                   otal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                    127863 seqs, 47026705 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
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SCN2_MESNA
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SCXC_CENLL
SCXC_LEIOH
SCX4_LEIOH
SCX4_LEIOH
SCX4_LEIOH
SCXE_LEIOH
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SCX7_MESNA
SIX2_LEIOH
SCX6_MITEN
SCX7_MESNA
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Maximum Match 100*
Listing first 45 summaries
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                                                                                                                                                                                                                                                                               Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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                                                                             TCCTGCGTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGTGAGTGCAAGAGGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01 JAN-1990 (Rel. 13, Last sequence update)
28 FEB 2003 (Rel. 41, Last annotation update)
Alpha-like neurotoxin ili (Bom 11:) (Bom3).
Buthus occitanus mardochei (Moroccan scorpion).
Eukaryota, Metazoa, Artiropoda, Chelicerata, Aradinida, Scorpiones;
Buthoidea, Buthidae, Buthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Venom; MeDLINE_87161829; PubMed=3104036; MeDLINE_87161829; PubMed=3104036; Vargas O., Martin M.-F., Rochat H.; Vargas O., Martinn of str toxins from the venom of the Moroccan "Characterization of structures from the venom of the Moroccan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
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US-39-673-274B-2 (1-169) x DEFN_HELVI (1-44)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a plicense agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb.ch).
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                                                                                                                                                                                               Toxin; Neurotoxin; Ionic channel inhibitor; Sodium channel inhibitor;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anti-neuroexcitation peptide II precursor (ANEPII).
Mesobuthus martensii (Manchurian scorpion) (Buthus martensii).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Mesobuthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99
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ANTI-NEUSCENCITATION PEPTIDE II.
BY SIMILARITY.
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CO45C7DACB3513AB CRC64;
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(Rel. 41, Last sequence update)
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InterPro; IPR002061; Scorpion_toxinL.
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85 AA;
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28-FEB-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 AspLysTyrThrGlyCysLysValTrpCysValIleAsnAsnGluSer---CysAsnSer 44
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Q9BKJ0; Q9G2C4;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Anti-neuroexcitation peptide III precursor (ANEPIII) (Anti-epilepsy
28-FEB-2003 (Rel. 41, Last annotation update)
Meurotoxin AS precursor.
Mesobuthus martensii (Manchurian scorpion) (Buthus martensii).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEUROTOXIN AS.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
A1286F9DDCD4FE90 CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003614; Knotl.
InterPro; IPR02061; Scorpion_toxinL.
Pfam; PP00537; toxin_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probom; PD000908; Scorpion_toxinL, 1.
SMART; SM00505; Knotl; 1.
Toxin; Neurotoxin; Signal.
19 POTENTIA!
                                                                                  Buthoidea; Buthidae; Mesobuthus
NCBI_TaxID=34649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF079060; AAD47374.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65
9759 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.00
55.81%
44.19%
25.93%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.0161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 Phecyscin 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VNB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ercent Similarity:
est Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P01492;
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DISULFID
DISULFID
SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Baloniformatics and the EMBL outstration the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license&isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

TISSUE-Bronm gland;
Zhang J.-H., Hua Z.C., Zhu D.X.;
Zhang J.-H., Hua Z.C., Zhu D.X.;
"Cloning of anti-neuroexcitation peptide III (ANEP) cDNA from Scorpion
Buthus martensii Karsch.";
Submitted (MAR-2000) to the EMBJ/GenBank/DDBJ databases.
-!- FUNCTION: Binds to sodium channels and inhibits them.
-!- SUBCELLULAR LOCATION: Secreted (By similarity).
                                                                                                                                                             SEQUENCE FROM N.A. TISSUE-Venom gland. Targus T.C. Zhu B.X.; Zhang J.-H., Hua Z.C., Zhu B.X.; "Cloning of anti-epilepsy peptide cDNA from scorpion Buthus martensi:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002061; Scorpion_toxind.
Pfam: PF00537; toxin 3; 1.
Profom: PD005098; Scorpion_toxind; 1.
PMMRT; SM00505; Knot1; 1.
Toxin; Neurotoxin; Ionic channel inhibitor; Sodium channel inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCTGCGTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGTGAGTGCAAGAGGAGG
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peptide).
Resobuthus martensii (Manchurian scorpion) (Buthus martensii).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Mesobuthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTTACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGCGAG 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- TISSUE SPECIFICITY: Expressed by the venom gland.
-!- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.
ALPHA-TOXIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
ANTI-NEUROEXCITATION PEPTIDE II
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                    Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases
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C1D6C93A2F82F8C2 CRC64;
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ą
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF122003; AAG01571.1; -. EMBL; AF242737; AAX28342.1; -. HSSP; P01494; 2SN3. InterPro; IPR003614; Knoti.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21
85
81
56
63
63
47
9271 XW,
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55.26%
42.11%
25.77%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 AA;
                                                                                                            NCBI_TaxID=34649;
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MEDLINE=96300228; PubMed=8706664;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   i6 CysPheTrpLeuGlyLysAsn----GluAsnCysAspLysGluCysLysAlaLysAsn 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 TACAAGGGT-----GGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGCGAG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochemistry 33:11135-11149(1994).

Biochemistry 33:11135-11149(1994).

Confidence of the activated channels, thereby blocking neuronal transmission.

Subcellular LOCATION: Secreted.

TISSUE SPECIFICITY: Expressed by the venom gland.

ETALLARTY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.

PIR, A55869, A55869.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49
                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=9524424; PubMed=7727365;
Lebreton F., Delepierre M., Ramirez A.N., Balderas C., Possani L.D.;
"Primary and NMR three-dimensional structure determination of a novel
crustacean toxin from the venom of the scorpion Centruroides limpidus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P01492; IVNB.
InterPro; PR000514; Knot1.
InterPro; IPR001519; Neurotoxin.
InterPro; IPR002061; Scorpion_toxinL.
Pfan, PR00251; toxin 3; 1.
Pr0Dom; PR002084; Scorpion_toxinL; 1.
Pr0Dom; PR005086; Scorpion_toxinL; 1.
SWART; SW00505; KnotL; 1.
Doxin; Neurotoxin; Ionic channel inhibitor; Sodium channel inhibitor.
01SULFID 12 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neurotoxin XIV precursor (Bot14).
Buthus occitamus tunetamus (Common European scorpion).
Eukaryota: Metazoa: Arthropoda: Chelicerata: Arachnida: Scorpiones;
Buthoidea: Buthidae: Buthus.
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Eukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Scorpiones,
Buthoidea, Buthidae, Centruroides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7338 MW; A478E63796F54DAA CRC64;
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                  SEQUENCE, DISULFIDE BONDS, AND STRUCTURE BY NMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [5-DEC-1998 (Rel. 37, Created)
15-DEC 1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                 01 NOV 1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
22+FEB-2003 (Rel. 41, Last annotation update)
crustacean-specific toxin 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09 673 274B-2 (1:169) x SCXC_CENLL (1-66)
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53.85
43.59
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TISSUE=Venom;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    limpidus Karsch.";
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                                                                                                                                                                                                                                                          NCBI_TaxID=29941;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                          TISSUE=Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
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Q17254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
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Query Match:
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                   Eur. 5. Blochem. 238:653-660(1996).

-!-FUNCTION: Binds to sodium channels and inhibits the inactivation of the activated channels, thereby blocking neuronal transmission. This toxin is active only on insects.
-!-SUBCELLUIAR LOCATION: Secreted.
-!-TISSUE SPECIFICITY: Expressed by the venom gland.
-!-SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.
ALPHA-TOXIN SUBFAMILY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Alpha-like neurotoxia IV (Bom IV) (Bom4).
Buthus occitanus mardochei (Moroccan scorpion).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones; Buthoidea; Buthus.
NCBI_TaxID=6869;
Bouhaouala-Zahar B., Ducancel F., Zenouaki I., Ben Khalifa R., Borchan L., Pelhate M., Boulain J.C., el Ayeb M., Menez A., Karoui H.;
                                                                         "A recombinant insect-specific alpha-toxin of Buthus occitanus tunetanus scorpion confers protection against homologous mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NEUROTOXIN XIV.
BY SIMILARITY.
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BY SIMILARITY.
4977F16C511F0567 CRC64;
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PIR; S68906; S68906.
InterPro; IPR030814; Knoti.
InterPro; IPR02081, Scorpion_toxini.
ProDom; PD000908; Scorpion_toxini.
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      STATE THE TEST AND DESCRIPTION OF THE PROPERTY OF THE PROPERTY
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               TISSUE-Venom;

MEDLINE-99203324; PubMed-10103091;

A Cestele S., Stanktewicz M., Mansuelle P., De Waard M., Dargent B., Gestele S., Stanktewicz M., Mansuelle P., De Waard M., Dargent B., Gestele S., Stanktewicz M., Mansuelle P., De Waard M., Dargent B., Gilles N., Pelhate M., Rochat H., Martin-Eauclaire M.-F., Gordon D.; "Scorpion alpha-like toxins, toxic to both mammals and insects, I feferentially interact with receptor site 3 on voltage-gated sodium in thannels in mammals and insects."; Eur. J. Neurosci. 11:975-985[1999].

C. - FUNCTION: Binds to sodium channels and inHibits the inactivation of the activated channels, thereby blocking neutronal transmission.

C. - FUNCTION: Binds to sodium channels and inHibitor. ALPHA-TOXIN SPECTRECT.

C. - TISSUE SPECIFICITY: Expressed by the venom gland.

C. - TISSUE SPECIFICITY: Expressed by the venom gland.

C. - TISSUE SPECIFICITY: Expressed by the venom gland.

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C. - TISSUE SPECIFICITY: Expressed by the Venom gland.

C. - FUNCTION: FAULTY: Expressed by the Venom gland.

C. - FUNCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90037062; PubMed=2808423;
Bougis P.E., Rochat H., Smith L.A.;
"Precursors of Androctonus australis scorpion neurotoxins. Structures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neuroccxii; Ionic channel inhibitor; Sodium channel inhibitor.

10 12 83 BY SIMILARITY.

10 22 46 BY SIMILARITY.

10 26 48 BY SIMILARITY.
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01.JUL-1993 (Rel. 26, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Neurotoxin III precursor (AaH III) (AaH3).
Androctonus australis hector (Sahara scorpion).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Butholdes; Buthidae; Androctonus.
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Kopeyan C., Martinez G., Rochat H.;
"Amino acid sequence of neurotoxin III of the scorpion Androctonus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of precursors, processing outcomes, and expression of a functional recombinant toxin II.";
SEQUENCE, PHARMACOLOGICAL CHARACTERIZATION, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4305EB32436A4B90 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              nuclear magnetic resonance assignments and secondary structure.";
J. Biomol. NMR 2:57-76(1992).
-!- FUNCTION: Binds to sodium channels and inhibits the inactivation
                                                             STRUCTURE BY NMR.
MEDUINE-91122921, PubMcd=2279844;
Laplante 5.R., Mikou A., Robin M., Guittet E., Delsuc M.A.,
Charpentier I., Lallemand J.-Y.;
"Rapid determination and NMR assignments of antiparallel sheets and
                                                                                                                                                                                                                                                                                                                                                                                                                      "Toxin III of the scorpion Androctonus australis hector: proton
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D -> N (IN REF. 2).
ADBOAD462153E3C CRC64;
                                                                                                                                                                                                                                                                                                  STRUCTURE BY NMR.
MEDLINE=91044377; PubMed-1422146;
Mikou A., Laplante S.R., Gilttet E., Lallerand J.-Y.,
Martin-Eauclaire M.-F., Rochat H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
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                                                                                                                                                                                                            helices of a scorpion and a cobra toxin.";
Int. J. Pept. Protein Res. 36:227-230(1990)
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InterPro, IPR003614, Knot:
InterPro, IPR002361, Scorpion_texinb.
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Eur. J. Biochem. 94:609-615(1979).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00537; tox:n 3;
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Gaps:
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Kopeyan C., Martinez G., Rochat H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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77.50
57.14%
38.10%
23.92%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 TrpCys 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
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Q9UACB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 GGTTACAAGGGTGGTCACTGCGGTTCCTTCGCT--- -- AACGTGAACTGCTGGTGC 126
                                                                                                                                                                                                                                                                                                                                                    MEDINE-22168983, PubMed=12180969,
MEDINE-22168983, PubMed=12180969,
Hamon A., Gilles N., Sautiere P., Martinage A., Kopeyan C., Ulens C.,
Tytgat J., Lancelin J.-M., Gordn D.,
"Characterization of scorpion alpha-like toxin group using two new
toxins from the scorpion Leiurus quinquestilatus hebraeus.";
Eur. J. Blochem. 269:3220-3933 (2002).
PUCTION: Binds to sodium channels and inhibits the inactivation
of the activated channels, thereby blocking neuronal transmission.
This toxin is highly toxic to insects and mice, and inhibits the
binding of alpha-toxin to cockroach membranes.
SUBCELLUIAR LOCATION: Secreted.
TISSUE SPECIFICITY: Expressed by the venom gland.
MISCELLANBOUS: LD(56) is 34.3 nmol/kg to cockroaches (Blatella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 GlyGlyThrGlyGlySisCysGlyPheLysLeuGlyH.sGly:leAlaCysTrpCys 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ptam; PF36537; toxin 3; 1.
PicDom; PD00968; Soorpion_toxin2; 1.
SmART: SM00505; Knotl; 1.
Toxin; Neurotoxin; Ionic channel inhibitor; Sodium diannel inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
26-FEB-2003 (Rel. 41, Last annotation update)
26-FEB-2003 (Rel. 41, Last annotation update)
Neurocoxin IV (Lqq IV) (Lqq4).
Leiutus quinquestriatus quinquestriatus (Egyptian scorpion).
Exiatyota: Metazoa; Arthopoda; Chelicerata; Arachnida; Scorpiones;
Burhoidea; Buthidae; Leiurus.
                                                                                                                                                   Leiurus quinquestriatus hebraeus (Yellow scorpion).
Eukaryota, Metazoa, Arthopoda, Chelicerata, Arachnida, Scorpiones;
Buthordea, Buthidae, Leiurus.
NCBI Taxib=6884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             germanica).
!- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCCRPION TOXIN FAMILY.
ALPHA-TOXIN SUBFAMILY: ALPHA-LIKE TOXIN SUBCLASS.
                                                                                                                                                                                                                                                                                                      SEÇUENCE, PHARMACOLOGICAL CHARACTERIZATION, AND BICASSAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49A54B0B6C75392E CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
                                                   28 FEB 2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Alpha-like neurotoxin Lqh VI (Lqh6).
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AMIDATION.
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     64 FB.
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34
44
46
64
6803 MW;
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     STANDARD;
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Best Local Similarity:
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Pred. No :
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P01489,
     SC16_LEIQH
P59356;
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SCX4_LEIQU
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70 AGGAGGGGTTACAAGGGTGGTCACTGC-----GGTTCCTTCGCTAACGTGAACTGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 AsnCysVallyrThrCysGlySerAsnSerTyr-----CysAsnThrGluCysThr 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 LysAsnGlyAlaGluSerGlyTyrCysGlnTrpLeuGlyLysTyrGlyAsnAla---Cys 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 TCCTGCGTGTGG-----GGTGCTGTGAACTACACTTCCGATTGCAACGGTGAGTGCAAG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neurotoxin AS-1 precursor.

Mesobuthus martensii (Manchurian scorpion) (Buthus martensii).

Eukaryota: Merazoa; Arthroppda; Chelicerata; Arachnida; Scorpiones;

Buthoidea; Buthidae; MeBobuthus.
"Primary structure of toxin IV of Leiurus quinquestriatus quinquestriatus.";
quinquestriatus.";
FEBS Lett. 181:211-217(1985).
                                                                                                                                                                                                                                                                                                                                               651
80 0 4
                                                                                                                                                                                                                                                                                                                                                                     Conservative:
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 A.A
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Matches:
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us-09-673-274b-2.rsp

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PIR; B34123; B34123.
HSSP; PC1494; 2SN3.
                                                                                                                                                                                                                                                                                             61 AA;
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Best Local Similarity:
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P09982;
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               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
                                                                                                                                                                                                                                                                                                                                                                                          1 GATAAGCTTATCGGTTCCTGCGTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGT 60
                                                                                                                                                                                                                                                                                                                                                                                                                 44
                                                                                                                                                                                                                                                                                                                                                                                                              26 AsnLysTyrThrGlyCysLysIleTrpCysValIleAsnAsnGluSer---CysAsnSer
                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GAGTGCAAGAGGAGGGTTACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Insect toxin 2 (Insect toxin Lqq172).

Leiurus quinquesiriatus quinquestriatus (Egyptian scorpion).

Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthodea; Buthidae; Leiurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Primary structure of scorpion anti-insect toxins isolated from the venom of Leiurus quinquestriatus quinquestriatus."; FEBS Lett. 261:423-426(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kopeyan C., Mansuelle P., Sampieri F., Brando T., Bahraoui E.M.,
Rochat H., Granier C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93160530; PubMed=8431601;
2lotkin E., Gurevitz M., Fowler E., Adams M.E.;
"Depressant insect selective neurotoxins from scorpion venom:
                                                                                                                                                                                           POTENTIAL.

BY CHIMLARITY.

BY SIMILARITY.

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EZ227488439E2B95 CRC64;
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Matches:
Conservative:
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Indels:
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                                                                                                                           InterPro; IPR003614; Knotl.
InterPro; IPR00261; Scorpion_toxinL.
Pfam. PF00537; toxin 3; 1.
ProDom; PD000908; Scorpion_toxinL; 1.
SWART; SM00505; Knotl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                        EMBL; AF079061; AAD47375.1; -.
                                                                                                                                                                                                      85
81
56
63
65
9802 MW;
                                                                                                                                                                                     Neurotoxin; Signal.
                                                                                                                                                                                                                                                                                         0.119
77.00
53.49%
39.53%
23.77%
ALPHA-TOXIN SUBFAMILY
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31
35
46
46
AA;
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uery Match:
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                                                                                                                                                                                                                                                                                                                ercent Similarity:
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P19855;
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--- FUNCTION: Binds to sodium channels and inhibits the inactivation of the activated channels, thereby blocking neuronal transmission. Has paralytic activity in mice.
--- SUBCELLULAR LOCATION: Secreted.
--- TISSUE SPECIFICITY: Expressed by the venom gland.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCTGCGTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGTGAGTGCAAGAGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 SerCysLeuPheGly----- AsnGluGlyCysAsnLysGluCysLysSerTy:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sodium channel inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGTTACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGGCGAG 12%
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Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Mesobuthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyGlySerTyrGlyTyrCysTrpThrTrp---GlyLeuAlaCysTrpCysGlu 45
                                                                         Ziotkin E., Fowler E., Eitan M., Moyer M., Adams M.E.;
"On the chemistry and action of the depressant insect toxins.";
Toxicon 28:170-170(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-85046632; Pubmed-6497916;
Volkova T.M., Garsia A.F., Telezhinskaya I.N., Potapenko N.A.
Grishin E.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
80F01771C7DCFAF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
chemistry, action, and gene cloning.";
Arch. Insect Biochem. Physiol. 22:55-73(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-1989 (Rel. 10, Created)
02-MAR-1989 (Rel. 10, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neurotoxin M14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Toxin; Neurotoxin; Ionic channel inhibitor: DISULFID 10 60 BY SIMILARITY. DISULFID 14 35 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-673-2748-2 (1-169) x SIX2_LEIQU (1-61)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ProDom; PD000908; Scorpion_toxinL; 1. SMART; SM00505; Knoti; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                InterPro, IPR003614; Knotl.
InterPro, IPR002061; Scorpton_toxinh.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6860 MW;
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76.50
55.268
39.478
23.618
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"A cis-trans isomerism of a non-prolyl peptide bond in LQH III alpha-
like scorpion toxin revealed by solution NMR.";
                                                                                                                                                                                                                                                                                                                                                                       Sodium channel inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   956678;
15-UUL 1999 (Rel. 38, Created)
15-UUL 1999 (Rel. 38, Last sequence update)
15-SEP-2063 (Rel. 42, Last annotation update)
Alpiral ike neuroroxin Lqh III (Lqhia)
Leiurus quinquestriatus hebraeus (Yellow scorpion)
Eukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Scorpiones;
Buthordea, Buthidae, Leiurus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "NVR structures and activity of a nove; alpha-like toxin from the scorpion Leiurus quinquestriatus hebraeus."; Mol. Biol. 285:1749-1763(1999).
-:- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.
ALPHA-TOXIN SUBFAMILY.
PIR; JT0020; NTSR4E.
HSSP; P45697; ISN1.
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Sautiere P., Cestele S., Kopeyan C., Martinage A., Drobecq H.,
Ecljansky Y., Gordon D.;
New toxins acting on sodium channels from the scorpion Leturu
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BEGDB42237EF2E8 CRC64;
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TOXIN; NeurotoXIN; Ionic channel
DISULFID 12 65 BY S
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Toxicon 36:1141-1154(1998).
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TISSUE=Venom;
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:D _SCL3_LEIQH
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11 AsnCysValTyrHisCysPheProGlySerSerGlyCysAspThrLeuCysLysGluLys 30
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Submitted (JUL-2003) to the PDB data bank.

-!- FUNCTION: Binds to sodium channels and inhibits the inactivation of the activated channels, thereby blocking neuronal transmission. Active on both insects and mammals but competes for alpha-toxins binding only on cockroach sodium channels.
-!- SUBMINIT: Monomer.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed by the venom gland.
-!- MISCELANEOUS: LD [50] is 50 mg/kg by intracerebroventricular injection into mice.
-!- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.
ALPHA-TOXIN SUBFAMILY. ALPHA-LIKE TOXIN SUBCLASS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 GlyGlyThrSerGlyHisCysGlyPheLysValGlyHisGlyLeuAlaCysTrpCys 49
                                                                                                                                                                                                                                                                                                                                                                                                                        Toxin; Neurotoxin; Ionic channel inhibitor; Sodium channel inhibitor;
Amidation; 3D-structure.
DISULFID 12 65
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00537; toxin 3; 1.
ProDom; PD000950; Scorpion toxini; 1.
SWART; SMC505; Knot1; 1.
                                                                                                                                                                                                                                                                    PDB; 1BMR; 16-FEB-99.
PDB; 1FH3; 08-NOV-00
InterPro; 1PR035614; Knot1.
InterPro; 1PR002061; Scorpion_toxinL.
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091670 leishmanna
09vzr2 drosophila
08wry4 centruroide
09dua7 mesobuthus
09vzr3 drosophila
09fp09 mesobuthus
09fp01 phaseolus a
09fp01 phaseolus a
09fp01 phaseolus a
09fp01 phaseolus a
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0813a6 caenorhabdi
0813a7 caenorhabdi
09xwd6 caenorhabdi
09xvd6 drosophila
09y08 mesobithus
039403 brassica ca
03uk6 drosophila
                                                    QBtito mesobuthus
PB2761 arabidopsis
Q9vzq5 drosophila
Q8mvs7 leiurus qui
                                                                                                                                                                                                                                                                                                                                                                                                                                                 015038 homo sapien
060382 homo sapien
Q9uha8 homo sapien
09uq35 homo sapien
09twll centrurolde
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Q8vhs2 mus musculu
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Q9whf2 agrotis seg
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O76963 orthochirus
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026292 leiurus qui
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Q17230 mesobuthus
Q8iOk7 mesobuthus
Q95wx6 mesobuthus
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Zhu X., Zhang T., Zhu Y.;
Zhu X., Zhang T., Zhu Y.;
"Cloning and sequencing of two depressant insect selective neurotoxin cDNAs from Buthus narteeris! Karsch.";
Kexue Tongbao 41:1367-1391(1996).
-!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mesobuthus martensii (Manchurian scorpion) (Buthus martensii).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Mesobuthus.
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Last annotation update)
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08T3TC
08T3TC
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08WZG
09Y1U3
09WZR2
09WZR2
09GWRY4
09GCR3
09GCR3
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09U.K6
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0810X7
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Q8MVS8
Q9Y0A9
Q8T3A6
Q9XWD6
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Q9UHA8
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01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2003 (TrEMBLrel. 23,
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 PRELIMINARY;
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 Insect toxin 2.
 017231
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OMDEL=frame+ n2p-model - DEV=x1p

O=/Cgn2_1/USFTO_epool/US09673274/runat_16102003_170627_2545/app_query.fasta_1.654

D=SCPTREMBL_23 -QFM=fasta. -SURFIX=rspt -MINNATCH=0.1 -LOOPCL=0 -LOOPEXT=0 - DEVEXT=0 - DEVEXTERMBL_23 -QFM=fasta. -SURFIX=rspt -MINNATCH=0.1 -LOOPCL=0 -LOOPEXT=0 - DOCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL OUTFWT=pct -NORM=ext -HEAPSIZE=550 -MINLEN=0 -MAXLEN=2000000000 - USR=US09673274 @CGN 1 1 216 @runat_16102003 170627_2545 -NCPU=6 -ICPU=3 NO MAAP -LARGEQUERY -NGE_GSCORESAO -MAIT -DSPBLOCK=10 -LONGLOG - GRAPOP=6 PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0 -THREOUS-1 -XGAPEXT=0 -SFGAPOP=6 -DELEXT=7
                                                                                          October 16, 2003, 17:06:37; Search time 49.9701 Seconds (without allgaments) 1745.479 Million cell updates/sec
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           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                 - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                      otal number of hits satisfying chosen parameters:
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4: sp_human:*
5: sp_invertebrate:*
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5: sp_mneamal:*
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Best Local Similarity:
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01-MAR-2003
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AA Zhu X., Zhang T., Zhu Y.;
An and sequencing of two depressant insect selective neurotoxin and sequencing of two depressant insect selective neurotoxin and sequencing of two depressant insect selective neurotoxin an archaematrensia karsch.";
CECHARS from Buthus martensia (Karsch.");
Kexue Tongbao 41:1387-1391(1996).
C. : SUMILARITY: BELONGS TO THE ALPHA/BETA·SCORPICN TOXIN FAMILY.
DR RASSP; POL494; 1837.
DR RASSP; POL494; 1837.
DR RICEPPO; IPRO3044; Mobi.
CR InterPro; IPR031219; Neurotoxin.
DR InterPro; IPR031219; Neurotoxin.
DR PRINTS: PR00284; TOXIN.
DR PRINTS: PR00284; TOXIN.
CR SHOUSH; SMO0199; SCORPION_TOXINL; I.
CR SMART; SMO0509; Knotl; I.
CR SMART; SMO0509; Knotl; I.
CR SMART; SMO1979.
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Bukaryota, Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Mesobuthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 GGTTACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGCGAG 129
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                                                                                                                               7285 MW; F13FCD7153855626 CRC64;
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Last annotation update)
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Matches:
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Matches:
InterPro; IPR001219; Neurotoxin.
InterPro; IRR002061; Scorpion_toxinL.
Pfam; PF00537; toxin 3: 1.
PRINTS; PR0284; TOXIN.
ProDom; PD00908; Scorpion; toxinL; 1.
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01 NOV-1996 (TrEMBLrel. 01,
01-MAR-2003 (TrEMBLrel. 23,
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                                                                                                           SMART; SM00505; Knotl;
SEQUENCE 65 AA; 7285
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Best Local Similarity:
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Best Local Similarity:
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scorpion
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Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Mesobuthus.
NCBL TaxID=34649;
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01-DEC-2001 (TrEMBLrel. 19, Last equence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Depressant insect neurotoxin BmK ITb precursor.
Mesobuthus martensii (Manchuian scorpion) (Buthus martensii).
Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones; Buthoidea; Buthidae; Mesobuthus.
76 GGTTACAAGGGTGACACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGCGAG 129
                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-221768B; Pubmed=1223055B;
MEDLINE-2221768B; Pubmed=1223055B;
MEDLINE-2221768B; Li M.X., Zhu Z.H., Liu H.;
Zeng K.C., Zeng X.C., Wa X.H., Pu J., Li W.X., Zhu Z.H., Liu H.;
"Molecular cloning and functional expression of a gene encoding an antiarrhythmia peptide derived from the scorpion toxin.";
EMBL; 2.B. 2.cohem. 269:4468-4475(2002).
EMBL; AR559791; AANS9783.1;
EMBL; AF559792; AANS9783.1;
                         diyalaTyrTyrGlyTyrCysTrpThrTrp---GlyLeuAlaCysTrpCysGlu 46
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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PubMed=11437247;
Vancosthuyse V., Miege C., Dumas C., Cock J.M.;
"Two large Arabidopsis thaliana gene families are homologous to shassica gene superfamily that encodes pollen coat proteins and
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6CF567086332001A CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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85 AA;
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NCBI_TaxID=3702;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Mesobuthus martensii (Manchurian scorpion) (Buthus martensii).
Bukaryota, Metazoa, Arthropoda; Chelicerata; Arachnida; Scorpiones;
NCBI_TAXID=34649;
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    POTENTIAL.
DEPRESSANT INSECT NEUROTOXIN BMK ITB.
80CDD3914956DE8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ling M.H., Wang C.G., Wang D.C., Chi C.W.;
Ling M.H., Wang C.G., Wang D.C., Chi C.W.;
Submitted (MAY-1998) to the EMBL/Genbank/DDBJ databases.
-- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
-- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.
EMBL; AF064821; AAD31592.1;
-- SIMILARITY: MELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.
HSSP; PO19494: 25833.
InterPro; IPR003614; Knot1.
InterPro; IPR002061; Scorpion_toxinL.
Propom; PD000908; Scorpion_toxinL, 1.
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CCE46711BAF21DAC CRC64;
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SEQUENCE 85 AA; 9330 MW;
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36.84%
25.15%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00505; Knot1; 1.
Neurotoxin; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                           ercent Similarity:
lest Local Similarity:
Nery Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sest Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ercent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lignment Scores:
                                                                                            lignment Scores:
red. No.:
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SEQUENCE
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Q9XYB7

ESULT 5

à

Muery Match:

8

á

red. No.:

core:

QBT3T0

RESULT 6

SIGNAL

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16 TCCTGCGTGTGGTGCTGTGAACTACACTTCCGATTGCAACGGGTGAGTGCAAGAGGAGG 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Miyajima N., Tabata S.;
"Structural analysis of Arabidopsis thallana chromosome 5. IX.
Sequence features of the regions of 1,011.550 bp covered by seventeen
Pl and TAC clones.";
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 23, Last annotation update)
Depressant insect toxin BmK Tral precursor.
Mesobuthus martensii (Manchurian scorpion) (Buthus martensii).
Eukaryota; Metacoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Mesobuthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the
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                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Liu Z., Chi C., Wu X.;

Liu Z., Chi C., Wu X.;

Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

Submitted (MAR-2002) SECRETED (BY SIMILARITY).

-! SUBCELLULAR LCCATION: SECRETED (BY SIMILARITY).

-! SIMILARITY: BELONGS TO THE ALPHA/RETA-SCORPION TOXIN FAMILY.

InterPro: JR003814; Knorl.

InterPro: JR003814; Knorl.

InterPro: JRC02061; Scorpion_toxinL.

ProDom; PD000998; Scorpion_toxinL.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 GGTTACAAGGGTGACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CV. COlumbia;
MEDLINE=99397451; PubMed=10470850;
Kaneko I., Katoh I., Sato S., Nakamura Y., Asamizu E., Kotani
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RESULT 9
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      Adams M.D. Ceiniker S.E. Holt R.A. Evans C.A., Gocayne J.D.,
RAD Adams M.D. Ceiniker S.E. Holt R.A. Evans C.A., Gocayne J.D.,
RAD Admaratides P.G., Scherer S.E. Li P.W. Hoskins R.A., Gatle R.E.,
Recorge R.A. Lewis S.E., R.Chards S. Ashburner M., Henderson S.N.,
RAD George R.A. Lewis S.E., R.Chards S. Chang C., Chen L.X.,
RAD George R.A. Basule R.W. Wandell M.D., Zhang C., Chen L.X.,
RAD Bardon R.C., Rogers Y.-H.C., Blazal R.C., Chang C., Chen L.X.,
RAD Bardon R.W., Bernan B.P., Morteel B.E., Kodira C., Katl C., McLeod M.P., McPherson D., R.A., Mowll S.M., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Suran S., Pollard B.P., Shen B., Shen B., Shen B.C., Scheeler F., Shen H. R., Rebern B.P., Shen B., Shen B., Shen B.C., Scheeler F., Shen H.
                                                                                                                                                                                                                                                                           16 TCCTGCGTGTGGGGTGCTGTGAACTACACTTCCGATTGCAAGGGTGAGGGAAGAGAGGG 75
                                                                                                                                                                                                                                                                                                         31 Thi CysLeuProGlyGluCysThi AsnProSerGluCysAshAlaAlaCysLysSerAsn 50
                                                                                                                                                                                                                                                                                                                                                                                                                                             090%C5;
01-CXT-2000 (TrEMBLrel. 13, Created)
01-CXT-2002 (TrEMBLrel. 22, Last sequence update)
01-CXT-2003 (TrEMBLrel. 23, Last annotation update)
CG32274 protein
CG32274 protein
CG32268 OR CG10815 OR CG1150.
CG32268 OR CG10815 OR CG1150.
CG3220011a melanogaster (Fruit fly).
Dusophila melanogaster (Fruit fly).
Bukaryota: Metaroa, Atthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachyceta; Muscomorpha;
                                                                             HYPOTHETICAL PROTEIN LCR46
male component of the self-incompatibility response. Plant Mol. Biol. 46:17-34(2001).
EMBL, AB017061; -; NOT_ANNOTATED_CDS.
Hyporhetical protein; Signal.
                                                                                             10BDEAAE80969F55 CRC64;
                                                                                                                                      Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                       76 GOTTACAAGGGTGGTCACTGCGGTTCCTTTCGCT 108
                                                                                                                                                                                                                                                                                                                                                       Z
                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ephydroidea, Drosophilidae, Drosophila
NCBI TaxID=7227;
                                                             POTENTIAL
                                                                                                                                                                                                                                               US:09-673-274B-2 (1:169) x P82761 (1-91)
                                                                                           91 AA; 9503 MW;
                                                                                                                                      0.123
80.00
58.06%
45.16%
24.69%
                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
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                                                                                                                        Alignment Scores:
Pred. No.:
                                                                                             SEQUENCE
                                                                                                                                                                                               Query Match:
DB:
                                                               SIGNAL
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                                                                               CHAIN
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    FREZERS
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13 GGTICCTGCGTGTGGGGGGGGTGCTGTGAACTTCCGATTGCAACGGTGAGGGGG 72
                                                                                                                                                                                                                                                                                                                                     Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
Celniker S.E., Adams M.D., Amanatides P.G., Barandon K.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon C., Beeson K.Y., Busam D.A.,
Carlson J.H., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
Ferriera S., Frise E. Adale R.F., Garge N.S., George R.A.,
Conzalez M., House C., Hoskins R.A., Hostin D., Howland T.J.,
McIntosh C.C., Moy M., Wurphy B., Nelson C., Nelson K.A., Nunco J.,
McIntosh C.C., Moy M., Wurphy B., Nelson C., Nelson K.A., Nunco J.,
Acteb J., Paragas V., Park S., Parel S., Pfeiffer B.,
Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
Alliams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,
Sequencing of Drosophila melanogaster genome.",
Sequencing of Drosophila melanogaster genome.",
Submitted (MAR-2001 to the EMBL/GenBank/DDBJ databases.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 AGGGGTTACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGCGAG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 GlySerCys-----AlaValTrpHisArgLysLysCysValAspIleCysGlnArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 GluGlyArgThrSerGlyHisCysSer-----ProSerLeuLysCysTrpCysGlu 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K., Hradecxy P., Huarg Y., Kaminker J.S., Prochnik S.B., Smith C.D., Tupy V.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Milburn G., Richter J., Russo S., Searle S.M., Smith E., Shu S., Smutnak F., Whiffield E., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., "Annotation of Drosophila melanogaster genome.", Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Massarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhao G., Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.(Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., "The genome sequence of Drosophila meianogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases. RMBL; AE003477; AAF47764.2; -. HSSP; P41964; IMYN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PD002594; Gamma-thionin; 1.
: 69 AA; 7722 MW; 87CC05D254A11AC4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6944
694
40
69
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lyBase; FBgn0052268; CG32268.
nterPro; IPR002118; Gamma-thionin.
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78.50
51.28%
41.03%
24.23%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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Pred. No.:
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19105 MW;
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75.00
41.79%
32.84%
24.75%
                                                                     0.351
76.50
55.26%
36.84%
23.61%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Myler P.J.;
Submitted (FEB-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
                                                                                                                                                                      Best Local Similarity:
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                                                                                                                                    Percent Similarity:
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                                       Alignment Scores:
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DB:
                                                                            Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 SerCysLeuPheGly------AsnGluGlyCysAsnLysGluCysLysSerTyr 49
                                                                                                                                                                                                                                                                                                                                     ZAKI T.I., Maruniak J.E.;

"Three polymorphic genes encoding LqqIT2 from the Egyptian scorpion Lelures quinquestriatus";

Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

-- SIMICHARITY: BELDNGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.

EMBL, AF474984; AAM-40281.;

InterPro; IPR003614; Knot1.

InterPro; IPR003614; Knot1.

InterPro; TPR003614; Scorpion_toxinL.

Pfam; PF00537; toxin 3; 1.

ProDom; PD000908; Scorpion_toxinL; 1.

SMART; SM00505; Knot1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ITČ.
Mesobuthus martensii (Manchurian scorpicn) (Buthus martensii).
Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Mesobuthus.
                       01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 23, Last annotation update)
Depressant insect toxin 2, Last annotation update)
Leiurus quinquestriatus quinquestriatus (Egyptian scorpion)
Eukaryota, Metazoa, Arthropoda, Chelicerata; Arachnida; Scorpiones;
NCBI_TaxID=6885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 GlyGlySerTyrGlyTyrCysTrpThrTrp---GlyLeuAlaCysTrpCysGlu 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 GGTTACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ling M., Wang C., Wang D., Chi C.;
Submitted (JUN 2000) to the EMBL/GenBank/DDBJ databases.
-- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY)
-- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY
EMBL; AF073899; AAD41648.2; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
DEPRESSANT INSECT NEUROTOXIN.
18E02CD791F3B5EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9099 MW; F13D53B18CDECBF0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82
12
2
2
2
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Depressant insect neurotoxin precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003614; Knotl.
InterPro; IPR002061; Scorpion_toxinL.
Pfam, PF00537; toxin_3; 1.
ProDom; PD000908; Scorpion_toxinL; 1.
SMART; SM00505; Knotl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JS-09-673-274B-2 (1-169) x Q8MVS7 (1-82)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85 AA; 9480 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.35
76.50
55.26
39.47
23.61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
3est Local Similarity:
2 Dery Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neurotoxin; Signal
                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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SEQUENCE
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34 SerCysLeuTrp3.y------AsrAspPheCysAspLysValCysLysLysSer 49
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                                                                                                                                                                                                                                                                                                                                                                                                                16 TCCTGCGTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGTGAGTGCAAGAGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 LeuSerLeuSerThrAlaAlaValArgArgSerArgAlaSerProProLeuAlaProThr
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Leishmania major.
Eukaryota; Euglenczoa; Kinetcplastida; Trypanosomatidae; Leishmania.
N.SB_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 GGTTACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGCGAG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99
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STRAIN=FRIEDLIN.
STRAIN=FRIEDLIN.
Myler P.J., Sisk E., Hixson G., Kiser P., Rickel E., Hassebrock Cawthra J., Marsolini F., Sunkin S., Stuart K.D.,
Submitted (FEB-2001) to the EMBL/GenBank/DDB databases.
-- SIMILARITY BELONGS TO THE LIBE FAMILY OF RIBOSOMAL PROTEINS EMBL, ACCOS802; AAF11045.1; --
InterPro, 18C00502; AAF11049.1; --
InterPro, IPRC02675; Ribosomal Libe.
ProDom; PF01781; Ribosomal Libe. 1.
Ribonucleoptotein; Ribosomal Libe: 1.
Ribonucleoptotein; Ribosomal France Fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to the EMBL/GerBank/DDBJ databases
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22
6
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19
20
3
    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2033 (TrEMBLrel. 23, Last annotation update)
Ribosomal protein L38.
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Matches:
Conservative:
Mismatches:
Indels:
Length:
Matches:
Conservative:
Mismatches:
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Alignment Scores:
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SIGNAL
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DB:
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                                                                                                                                                                                                                                                         Best Local
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No..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8WRY4
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RAINTEDERREEEEY,
RA Adarrs M.D., Celniker S.E., Holf R.A., Evais C.A., Gocayue J.D.,
RA Adarrs M.D., Celniker S.E., Holf R.A., Evais C.A., Gocayue J.D.,
RA Adarrs M.D., Celniker S.E., Richards S., Asrburner M., Henderson S.N.,
Barton G. Wortman J.R., Yandell M.D., Zhang O., Citen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazes, R.G., Neister B.D.,
RA Abril J.F., Benos P.V., Berrar E.G., Helf G., Neison C.R., Miklos G.L.G.,
RA Belkova D., Bercham M., Baxendale J., Brotater P., Bottler P.,
RA Belkova D., Bottler M.A., Benos P.V., Berrar B.P., Brottler P.,
RA Belkova D., Bottler M.A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Belkova D., Bottler A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Grerty M., Cabley S., Dallike C., Davenpolt L.B., Davies P.,
RA Grerty M., Evangelista C.C., Ferrar C., Errira G., Fleischman W.,
RA Godon K.J., Evangelista C.C., Ferrar C., Gelbart M.M., Glasser K.A.,
RA Godon K.J., Cabriellan A.E., Garg N.S., Gelbart M.M., Glasser R.A.,
RA Godon K.J., Cabriellan A.E., Garg N.S., Gelbart M.M., Glasser R.A.,
RA Harris M.L., Harvey D., Herman T.J., Hernandez J.R., Houck J.,
RA Harris M.L., Harvey D., Kraft C., Mortis J., Moshrefi A.,
RA Belson D.W., Puttoman G.S., Pan S., Pellact F., Shen H.,
RA Belson D.W., Murphy B., Murphy L., Wardy L.M., Nilson D.L.,
RA Belson D.W., Murphy B., Murphy L., Wardy E.M., Nilson D.L.,
RA Belson D.W., Murphy B., Murphy L., Wardy E.M., Wardy E.M.,
Rabeson R., Pittman G.S., Pan S., Pellact F., Shen H.,
Rabeson R., Musch M., Murphy B., Murphy L., Wardy E.M., Wardy E.M.,
Rabeson R., Pittman G.S., Pan S., Pellact E., Spradina A., San D., Rabesen M.G.,
Rabeson R., Wassarman D.A., Welley K., Wu D., Yang S., Yao Q.A.,
Rabeson R., Wassarman D.A., Welley K., Wu D., Yang S., Yao Q.A.,
Rabeson R., Wassarman D.A., Welley K., Wu D., Yang G., Rull R.F., San D.,
Rabe
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Staplaton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
Ceiniker S.,
                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).

Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.

NCBI_TaxID=7227,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-2002) to the EMBL/GenBark/DDBJ databases.
EMBL; AE003477; AAF47757.1; --
EMBL; AY118762; AAMS0622.1; --
HSSP; P41964; IMYN.
                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                      $
                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
.....CAGCACCC 26
                                                     73 PheSerProLeuGluHisPro 79
                                                                                                                                                                                                                                                                                                                 CG10812 protein (GH09576p).
                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                               CG10812
                                                                                                                                                                      Q9VZR2
Q9VZR2;
                                                                                                                RESULT 12
                                                                                                                                              C9VZR2
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31 CysThrLeuAlaCysIleAspLysThrGlyAspLysAsnCysAspArgAsnCysLysLys 50
                                                                                                                                                                                                                                                                             50 GluGluGiyArgSerSerGiyHisCysSer----ProSerLeuLysCysTrpCysGlu 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 TGCGTGTGGGGTGCTGTGAACTACACTTCCGAT-----TGCAACGGTGAGTGCAAGAGG 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 AGGGGTTACAAGGGTGGTGACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGCGAG 129
                                                                                                                                                                                                                                                              13 GGTTCCTGC - - GTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGTGAGTGCAAG
                                                                                                                                                                                                                                                                                                                               70 AGGAGGGGTTACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Centruroides limpidus limpidus (Mexican scorpion).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Centruroides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NA+-CHANNEL MODIFYING TOXIN.
21018F12E2ECC26E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72555FD8B1DCC6F7 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Na+-channel modifying toxin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                         Conservative:
Mismatches:
                                                                                                                       Matches:
                                                                                                      Length:
                                                                                                                                                                         Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR003614; Knot1.
InterPro; IPR002061; Scorpion_toxinL.
Pfam. PF0057; toxin_3; 1.
SMART; SM00508; Scorpion_toxint; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-673-274B-2 (1-169) x Q8WRY4 (1-84)
FlyBase; FBgn0035434; CG10812.
InterPro; IPR002118; Gamma-thionin.
ProDom; PD002594; Gamma-thionin; 1.
SEQUENCE 69 AA; 7656 MW; 72555F!
                                                                                                                                                                                                                          US-09-673-274B-2 (1-169) x Q9VZR2 (1-69)
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74.00
48.721
35.901
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74.50
42.50
37.50
22.99
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                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
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completed: October 16, 2003, 17:16:12
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SEQUENCE 106 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
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In W. X., Zeng X.-C., Zu S.-Y.;

In W. X., Zeng X.-C., Zu S.-Y.;

In W. X. Zubacted (MAY. 1999) to the EMBL/GenBank/DBJ databases.

L. Submitted (MAY. 1999) to the EMBL/GenBank/DBJ databases.

-!- SUBCELLULAR LOCATION: SECEPTED (BY SIMILARITY)

R. REBL, #5150009, AAG09657.1; -.

R. HSSP; P1728; 1LQI.

R. InterPro: IPR001219; Neurotoxin.

R. InterPro: IPR001219; Neurotoxin.

R. InterPro: IPR00261; Scorpion_toxin.

R. PRINTS; PR00284; TOXIN.

R. PRINTS; PR00284; TOXIN.

R. PRINTS; PR00289; Scorpion_toxinl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 TGCAACGGTGAGTGCAAGAGGGGGTTACAAGGGTGGTCACTGC-----GGTTCC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99
                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 15, Last annotation update)
Mypothetical 9.4 kba procein.
Hypothetical 9.4 kba procein.
Mesobuthus martensii (Manchurian scorpion) (Buthus martensii)
Ebkaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea: Buthidae; Mesobuthus.
51 GluGlyGlySerPheGlyHisCysSerTyrSerAla------CysTrpCysLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAX-2003 (TrEMBLrel. 23, Last annotation update)
01-MAX-2003 (TrEMBLrel. 23, Last annotation update)
CG10813 protein
CG33279 OR CG10813.
Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda; Insecta; Pterygota;
Behydroidea: Drosophilidae; Drosophila.
NCBI_TAXID=7227;
                                                                                                                                                                                                                                                                                                                          SMART; SM00505; Knot1; 1. Hypothetical protein. SEQUENCE 85 AA; 9426 MW; 6EFC463E02E95091 CRC64;
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Matches:
Conservative:
Mismatches:
Indels:
                                             85 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103 TTCGCTAACGTGAACTGCTGGTGC 126
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SEQUENCE FROM N.A.
TISSUE=Venom gland;
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est Local Similarity:
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RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,

Randon R.C., Rogers Y. H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Abril J.F., Agbayana A., An H.-J., Andrews-Pfannkoch C.R., Baldwin D.,

RA Ballew R.M., Baseu A., Baxendale J., Bayraktaroglu L., Besaley E.M.,

Ballew R.M., Baseu A., Baxendale J., Bayraktaroglu L., Besaley E.M.,

RA Borkova D. Bocchan M.R., Bouck J., Brokstein P., Brottler P.,

RA Borkova J.M., Cawley S., Dalke C., Davengor L.B., Chener A., Chandra J.

RA Cherry J.M., Cawley S., Dalke C., Davengor L.B., Davies P.,

RA Gerry J.M., Cawley S., Dalke C., Davengor L.B., Davies P.,

RA Durbin K.J., Evangalista C., Mays A.D., Dew I., Dietz S.M.,

RA Gloden K.J., Gong F. Gorrell J. H., Galler M.M., Glasser K.,

RA Glodek A., Gong F. Gorrell J. H., Guller M.M., Glasser R.,

RA Harris N.L., Harvey D., Heiman T.C., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.C., Hernandez J.R., Houck J.,

RA Alali M., Kalusi R., Kalusi T., Mar M., Libang Y., Lin X.,

Lasko P., Lei Y., Levitsky A.A., Li Z., Liang Y., Lin X.,

RA Liu X., Matter B., Wolliam D., Morised M.P., Morbreson D.,

Ra Melson D.R., Newlson K.A., Nicholy U., Morise J., Mossizefi A.,

Ralazzolo M., Patiens G., Staff C., Kravitz S., Liang Y., Lin X.,

Ralazzolo M., Patienna G.S., Pan S., Pollard J., Mossizefi A.,

Ralazzolo M., Patienna G.S., Pan S., Pollard J., Wolsen C.,

Shore E., Spradling A.C., Staffer R., Venter E., Wang X.,

Ralazzolo M., Patienna G.S., Pan S., Pollard J., Wang X.,

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Ralazzolo M., Patienna G.S., Pan S., Pollard J., Wang X.,

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Ralazzolo M., Patienna G.S., Pan S., Pollard J., Wang X.,

Ralazzolo M., Wassarman D.A., Weinstock M., Wang X., Yung X.,

Ralazzolo M., Wassarman D.A., Weinstock M., Wang X., Yung X.,

Ralazzolo M., Wassarman G.S., Zana M., Zhong W., Zhong 
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InterPro, IPRCC2118, Gamma-thionin.
InterPro, IPRC03614, Knct1.
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106 AA; 11598 WW;
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Best Local Similarity:
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us-09-673-274b-2.rag

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MODEL= frame+ n.p. model - DEV=xlp Q=/coll 16102603 170626 2523/app query.fasta_1.654 Q=/cgn2_1/USPTO_spool/US09673274/runat_16102603 170626 2523/app query.fasta_1.654 Q=/cgn2_1/USPTO_spool/US09673274/runat_16102603 170626 2523/app query.fasta_1.654 Q=/cgn2_1/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spool/USPTO_spoo
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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E	of a he	liomycin peptide.	
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KW Heliomycin; polycys: KW fungal infection; p KW transgenic plant; fi	teine pe lant pro ungi; ba	ptide; antifungal; antib tection; animal protection cteria; Cercospora betic rium culmorum; F. oxyspo	acterial; on; ola; ola;
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                                                                                                                                                                                    The present sequence represents the heliomycin peptide. Heliomycin is a polycysteine peptide with antifungal and antibacterial activity, isolated from the lepidopteron Heliothis virescens. Heliomycin peptides contain the sequence given in AAYS478. The heliomycin peptides contain the sequence given in AAYS478. The heliomycin peptides are used as pharmaceuticals for treating or preventing fungal infections in humans and animals. They may also be used as antifungal agents for plant protection. Nucleic acid encoding the heliomycin peptides is used to generate transgenic plants that are resistant to some fungil and bacteria (specifically Cercospora beticola, Cladosporium herbarum, Fesatium cullmorum, F. oxysporum and Phytophthora cinnamonii, and for recombinant production of the peptides.
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veterinary medicine; plant protection; bacterial infection;
                                                                                                                                    New polycysteine peptides, designated heliomycin, with antifungal antibacterial activity, useful in medicine or plant protection
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                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to peptide derivatives of heliomicine with annifungal and/or antibacterial activity. The present sequence is one such peptide. The peptides are useful in human and veterinary medicine and in plant protection, for control of bacterial and fungal infections. An antifungal and/or antibacterial composition containing at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AspLysLeuileGlySerCysValTrpGlyAlaValAsnTyrThrSerAspCysAsnGly
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antifungal agents in human or veterinary medicine and agriculture
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                                                                                                                                                                                                                                                                                                                              The present invention relates to peptide derivatives of heliomicine with antifungal and/or antibacterial activity. The present sequence is one such peptide. The peptides are useful in human and veterinary medicine and in plant protection, for control of bacterial and fungal infections. An antifungal and/or antibacterial composition containing at least one
                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                     GATAAGCTTATCGGTTCCTGCGTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGT
                                                       New peptide derivatives of heliomicine, useful as antibacterial and antifungal agents in human or veterinary medicine and agriculture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "residues derived from the yeast Mat-alphal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence of a fusion peptide of MF-alphal/heliomycin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mat alphal factor; MF-alphal; heliomycin; polycysteine peptide; antifungal; antibacterial; fungal infection; plant protection; animal protection; transgenic plant; fungi; bacteria; Cercospora beticola; Cladosporlum herbarum; Fusarium culmorum;
                                                                                                                                                                                                      4 4 0 0 0 0 0
4 4
                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "heliomycin residues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MF-alphal) factor"
                                                                                                                                                                                                                                                                     JS-09-673-274B-2 (1-169) x ABB76868 (1-44)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F. oxysporum; Phytophthora cinnamoni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - Saccharomyces cerevisiae.
- Heliothis virescens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                              AAY54374 standard; Peptide; 49 AA
                                                                                    Claim 15; Page 57; 100pp; French.
                    ä
                   Menin
                                                                                                                                                                                                    6.42e-26
267.00
100.00%
100.00%
82.41%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                      121 TGGTGCGAGACT 132
                                                                                                                                                                                                                                                                                                                                                                                        41 TrpCysGluThr 44
                                                                                                                                                      peptide is also claimed
                   Legrain M,
                                     4PI; 2002-179779/23
(ENTO-) ENTOMED SA.
                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
                                                                                                                                                                         44 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FR2777568-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-APR-1998;
                                                                                                                                                                                           Alignment Scores:
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                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric
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                                                                                                                                                                                                               score:
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The present sequence represents a fusion peptide of 5 amino acids derived from the Mar alphal factor (MF-alphal) and heliomycin. The attachment of the MF-alphal sequence to the N-terminal aids secretion of the heliomycin peptide. Heliomycin is a polycysteine peptide with antifungal and antibacterial accivity, isolated from the lepidopteron Heliothis virescens. Heliomycin peptides contain the sequence given in AXY54378. The heliomycin peptides are used as pharmaceuticals for treating or preventing fungal infections in humans and animals. They may also be used as antifungal agents for plant protection. Nucleic acid encoding the heliomycin peptides is used to generate transgenic plants that are resistant to some fungi and bacteria (specifically Cercospora beticola, Cladosporium herbarum, Fusarium culmorum, F. oxysporum and Phytophthora cinnamoni), and for recombinant production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GAGTGCAAGAGGAGGGGTTACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 AspLysLeulleGlySerCysValTrpGlyAlaValAsnTyrThrSerAspCysAsnGly 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GATAAGCTTATCGGTTCCTGCGTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 GluCysLysArgArgG;yTyrLysGlyG;yHisCysGlySerPheAlaAsnValAsnCys 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fungal infection; plant protection; animal protection; transgenic plant; fungi; bacteria; Cercospora beticola; Cladosporium herbarum; Fusarium culmorum; F. oxysporum; Phytophthora cinnamoni.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PR-lalpha; heliomycin; polycysteine peptide; antifungal; antibacterial;
                                                                                                                                                                                                           New polycysteine peptides, designated heliomycin, with antifungal or antibacterial activity, useful in medicine or plant protection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1..30
/note= "tobacco PR-lalpha signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fusion peptide of PR-lalpha signal peptide/hellomycin.
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Matches:
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                                                       (RHON ) RHONE-POULENC AGRECHIMIE
                                                                                                                                                                                                                                                                                                          Claim 13; Page 31; 46pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric - Nicotiana sp.
Chimeric - Heliothis virescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.54e-26
267.00
100.00$
100.00$
82.41$
98FR-0004933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 TGGTGCGAGACT 132
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                                                                                                                      2000-108532/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity:
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                                                                                                                         WPI; 2000-108532;
N-PSDB; AAZ45691
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15-APR-1998;
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61 GAGTGCAAGAGGAGGGGTTACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGC 120
                                                                                                                                                                                                                                                                                                          The present sequence represents a fusion peptide of the tobacco PR-lalpha signal peptide and heliomycin. The attachment of the PR-lalpha sequence to the N-terminal ands secretion of the heliomycin peptide. Heliomycin is a polycysteine peptide with annitungal and annibaccerial activity, isolated from the lepidopteron Heliomycin purescens. Heliomycin peptides contain the sequence given in AAY5437B. The heliomycin peptides are used as pharmaceuticals for treating or preventing fungal infections in humans and animals. They may also be used as antifungal agents for plant protection. Nucleic acid encoding the heliomycin peptides is used to generate transgenic plants that are resistant to some fungi and bacteria (specifically cercospora beticola, Cladosporum herbarum, Pusarium culmorum, F. oxysporum and Phytophthora cinnamoni; and for recombinant production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GATAAGCTTATCGGTTCCTGCGTGTGGGGTGCTGTAACTACACTTCCGATTGCAACGGT 60
                                                                                                                                                                                                                                       or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antifungal, antibacterial, fungicide, heliomicine, human medicine, veterinary medicine; plant protection, bacterial infection,
                                                                                                                                                                                                                                    New polycysteine peptides, designated heliomycin, with antifungal artibacterial activity, useful in medicine or plant protection
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4.4
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Matches:
Conservative:
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Indels:
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              "heliomycin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB76895 standard; Protein; 44 AA
                                                                                                                                                               (RHON ) RHONE-POULENC AGROCHIMIE
                                                                                                                                                                                                                                                                                 Claim 13; Page 32; 46pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.01e-26
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100.00%
100.00%
82.41%
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31...74
/note=
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Best Local Similarity:
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                                                                                                                                                                                              WPI; 2000-108532/
N-PSCB; AAZ45693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the peptides
                                                                                                     .5-APR-1998;
                                                                                                                                    15-APR-1998;
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                                             FR2777568-A1
                                                                         22-CCT-1999
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GAGTGCAAGAGGAGGGTTACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGC 120
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                                                                                                                                                                                                                                                                                                    The present invention relates to peptide derivatives of heliomicine with antifungal and/or antibacterial activity. The present sequence is one such peptide. The peptides are useful in human and veterinary medicine and in plant protection, for control of bacterial and fungal infections. An antifungal and/or antibacterial composition containing at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GATAAGCTTATCGGTTCCTGCGTGTGGGTGCTGTGAACTACACTTCCGATTGCAACGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AspLysLeulleGlySerCysValTrpGlyAlaValAsnTyrThrSerAspCysAsnGly
                                                                                                                                                                                                                                     New peptide derivatives of heliomicine, useful as antibacterial and antifungal agents in human or veterinary medicine and agriculture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antifungal, antibacterial; fungicide; heliomicine; human medicine; veterinary medicine; plant protection; bacterial infection;
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                             Disclosure; Page 86; 100pp; French.
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                                                                                                                                                                                    Menin L;
                                                                                                                13-JUL-2000; 2000FR-0609248.
19-SEP-2000; 2000FR-0011949.
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100.00%
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82.10%
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                                                                                                                                                                                                                                                                                                                                                                         peptide is also claimed
                                                                                                                                                                                    Legrain M,
                                                                                                                                                                                                         WPI; 2002-179779/23
                                                                                                                                                          (ENTO-) ENTOMED SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                   44 AA;
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                                     WO200206324-A2
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                                                             24-JAN-2002
                                                                                                                                                                                   Dimarcq J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
            Synthetic.
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24-JAN-2002

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Dimarcq J, Legrain M,
                                            Legrain M,
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                                                                                    WPI; 2002-179779/23
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(ENTC-) ENTOMED
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Pred. No.:
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                                               Dimarcq J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
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19-SEP-2000; 2000FR-0011949.
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                                                                                     New peptide derivatives of helionicine, useful as antibacterial and antifungal agents in human or veterinary medicine and agriculture
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                                                                                                                                                               Claim 15; Page 57; 100pp; French
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                                              The present invention relates to peptide derivatives of heliomicine with antifungal and/or antibacterial activity. The present sequence is one such peptide. The peptides are useful in human and veterinary medicine and in plant protection, for control of bacterial and fungal infections. An antifungal and/or antibacterial composition containing at least one
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helicmicine, useful as antibacterial and or veterinary medicine and agriculture
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New peptide derivatives of antifungal agents in human
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antifungal and/or antibacterial activity. The present sequence is one such peptide. The peptides are useful in human and veterinary medicine and in plant protection, for control of bacterial and fungal infections. An antifungal and/or antibacterial composition containing at least one peptide is also claimed.
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19-SEP-2000; 2000FR-0011949.
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The present invention relates to peptide derivatives of hellomicine with antifungal and/or antibacterial activity. The present sequence is one such peptide. The peptides are useful in human and veterinary medicine and in plant protection, for control of bacterial and fungal infections. An antifungal and/or antibacterial composition containing at least one peptide is also claimed.
                                                                                              GATAAGCTTATCGGTTCCTGCGTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGT
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                                                       US-09-673-274B-2 (1-169) x ABB76865
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Antifungal, antibacterial; fungicide; heliomicine; human medicine; veterinary medicine; plant protection; bacterial infection;

fungal infection.

WO200206324-A2.

Synthetic.

24-JAN-2002

Antifungal/antibacterial peptide pEM42

03-JUL-2002

ABB76865;

ABB76865 standard; Protein; 44 AA

ESULT 12 **BB76865**

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121 TGGTGCGAGACT 132 New peptide derivatives of heliomicine, useful as antibacterial and antifungal agents in human or veterinary medicine and agriculture

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Dimarcq J, Legrain M,

(ENTO-) ENTOMED SA.

WPI; 2002-179779/23

13-JUL-2000; 2000FR-0009248. 19-SEP-2000; 2000FR-0011949.

05-JUL-2001; 2001WO-FR02164

Claim 15; Page 57; 100pp; French.

444

Length: Matches: Conservative:

2.84e-25 262.00 97.73\$

Percent Similarity:

Alignment Scores:

peptide is also claimed.

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21 GluCysLysArgArgGly:?yrLysGlyGiyHisCysGlySerPheLeuAsnValAsnCys 40
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                     . AspLysieulleGlySerCysValTrpGlyAlaValAsnTyrThrSerAspCysAsnGly 20
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Sequence 6, Sequence 2,

Sequence Sequence

Sequence 8, Sequence 43

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Sequence 411. App
Sequence 410, App
Sequence 18. App
Sequence 18. App
Sequence 18. App
Sequence 18. App
Sequence 408, App
Sequence 404, App
Sequence 404, App
Sequence 418, App
Sequence 418, App
Sequence 418, App
Sequence 483, App
Sequence 396, App
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Sequence 23, Appl
Sequence 309, Appl
Sequence 339, Appl
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GENERAL INFORFATION:
APPLICANT: Allier: Danie; J.
APPLICANT: Herrmann, Rafael
APPLICANT: U., Albert J.
APPLICANT: Economic Billy F.
APPLICANT: Mcaver, Janues K.
APPLICANT: Presentil, James K.
APPLICANT: Mong, James K.
APPLICANT: Wong, Janues F. H.
TITLE OF INVENTION: Antimicrobial Polypeptides and Their
TITLE OF INVENTION: Antimicrobial Polypeptides and Their
TITLE OF INVENTION: Uses
FILE FEFFENCE: 35718/246215
CURRENT APPLICATION NUMBER: US/10/125,258
CURRENT FILING DATE: 2002-34-18
PRIOR APPLICATION NUMBER: 60/285,355
PRIOR FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 127
SEQ ID NO 119
LENGTH: 44
TYPE: PRI
5 US-10-125-258-119
5 US-10-125-258-119
6 US-10-126-4-480-11
105-10-10-126-4-480-11
105-10-10-126-4-480-12
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MODEL=frame+ n2p.model - DEV=Xlp

MODEL=frame+ n2p.model - DEV=Xlp

Q=/cgn2_1/USPrO_spool/US09673274/runat_16102003_170630_2743/app_query.fasta_1.654

DB=Published_Applications_AA - OFMT-fastan - SUFFIX=rapb - MINXATCH=0.1

LOOPCL=0 - LOOPEXT=0 - UNITS=bits - START=1 - ENN=-1 - MATRIX=bicsum62

LOOPCL=0 - LOOPEXT=0 - UNITS=bits - START=1 - ENN=-1 - MATRIX=bicsum62

THR MIN=0 - ALGN=15 - MODE=LOCAL_OUTPHT=pto - NORM=ext - HEAPSTZE=500 - MINLEN=0

MAXLEN=2000000000 - USER=US09673274 @CGN 1 1 106 @runat 16102003 170630_2743

MAXLEN=120 - MARN TIMEOUT=30 - THREADS=1 - SCRPED-0 - MINLEN=0

LONGLOG - DEV TIMEOUT=120 - WARN TIMEOUT=30 - THREADS=1 - SCRAPOP=10 - SCRAPEXT=0.5

FGAPOP=6 - FSÄPEXT=7 - YGAPOP=10 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
                                                                                                                                        October 16, 2003, 17:12:07; Search time 35.0914 Seconds (without alignments) 1578.850 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution.
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1 gataagcttatcggttcctg.....gaacgtgtcgacggatccgg 169
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1: /cgn2_6/ptodata/2/pubpaa/US37_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW PUB_FEP:*

3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

13: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

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17: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
                          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                     protein search, using frame_plus_n2p model
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Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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and is derived
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Result

Sequence 308, App Sequence 338, App Sequence 10081, Ap Sequence 677, App Sequence 1100, App

Seguence 783, App Seguence 147, App Seguence 3, Appli

Sequence 4, Appli Sequence 21, Appl Sequence 15, Appl

Sequence

12, Appi 208, App 168, App

Sequence 1 Sequence 2 Sequence

Seguence

Sequence 396, 7 Sequence 395, 7 Sequence 12, At

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Percent Similarity:
Best Local Similarity:
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US-10-12-2 139-117
US-10-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-2 139-12-
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Mismatches:
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US 10 125 258 117
/ ORGANISM: Agrotis ipsilon
US-10-125-258 119
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|TrpCysGlu 72
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RESULT 3

US-10-264-480-13

Sequence 13, Application US/10264480

Sequence 13, Application US/10264480

Bublication No. US20030113892A1

GENERAL INFORMATION:
TAPLICANT: Harmock, Bruce D.
TITLE OF INVENTION: SOCATED POLYPEPTIDES AND COMPOSITIONS

TITLE OF INVENTION: FROM THE VENOM CF P. TRANSVAALICUS AND METHODS OF USE

CURRENT APPLICATION NUMBER: US/10/264,480

CURRENT APPLICATION NUMBER: US/10/264,480

CURRENT APPLICATION NUMBER: GC/393,70

PRIOR FILING DATE: 2002-06-28

PRIOR FILING DATE: 2001-0-04

NUMBER OF SEQ ID NOS: 35

NUMBER OF SEQ ID NOS: 35

LENGTH: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-264-480-11

Sequence 11. Application US/10264480

Publication Nc. US20030113892A1

GENERAL INFORMATION:
APPLICANT: Harmock, Bruce D.
APPLICANTION: FROM THE VENOM OF P. TRANSVALICUS AND METHODS OF USE
CURRENT APPLICATION NUMBER: 60/333,070

PRIOR APPLICATION NUMBER: 60/333,070

PRIOR FILING DATE: 2002-06-28

PRIOR FILING DATE: 2002-06-28

PRIOR FILING DATE: 2001-10-04

NUMBER OF SEQ ID NOS: 30.

SEQ ID NO 11

SED ID NO 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 GinGlyGlySerTyrGlyTyrCysTyrAlaPheAla-----CysTrpCysGlu 49
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Indels:
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43.59%
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79.50
53.85%
43.59%
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, ORGANISM: Scolopendra canidens DS
US-09-829-481-2
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// Publication No. US20030167519A1
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APPLICANT: Inceeglu, Bora
TITLE OF INVENTION: ISOLATED POLYPEPTIDES AND COMPOSITIONS
TITLE OF INVENTION: FROM THE VENOM OF P. TRANSVAALICUS AND METHODS OF USE
FILE REFERENCE: UCAL256
CURRENT APPLICATION NUMBER: 00/1903,070
PRIOR APPLICATION NUMBER: 60/393,070
PRIOR APPLICATION NUMBER: 60/393,070
PRIOR FILING DATE: 2002-10-04
PRIOR FILING DATE: 2001-10-04
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 61
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| CysPheTrpLeuGlyLysAsn-----GluAsnCysAspLysGluCysLysAlaLysAsn 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCTGCGTGTGGGGGGGGTGCTGTGAACTACACTTCCGATTGCAACGGTGAGTGCAAGAGGAGG 75
                                                                      TGCGTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGTGAGTGCAAGAGGAGGGGT 78
                                                                                                                                             79 TACAAGGT-----GGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGCGAG 129
                                                                                                                                                                    34 GlnGlyGlySerTyrGlyTyrCysTyrSerPheAla------CysTrpCysGlu 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 GGTTACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGCGAG 129
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12
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ORGANISM: Leiurus quinquestriatus quinquestriatus
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Matches:
Conservative:
Mismatches:
Indels:
                                S-09-673-274B-2 (1-169) x US-10-264-480-11 (1-66)
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Patent No. US2002069427A1
GENERAL INFORMATION:
APPLICANT: Preenail, James
APPLICANT: Weng, Zude
APPLICANT: Wong, James
APPLICANT: Wong, Asmes
TITLE OF INVENTION: Arthropod Defensins
FILE REFERENCE: BB1441 US NA
CURRENT APPLICATION NUMBER: US/09/829,481
CURRENT FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: 60/17779
PRIOR FILING DATE: 2000-04-11
SOFTWARE: Microsoft Office 97
SEQ ID NOS: 11
SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps:
   Gaps:
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76.50
55.26
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    Percent Similarity:
    Best Local Similarity:
    Duery Match:
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Disease-Resistant
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                                                                                                                                                                                                                                                                                       34 GluCysAsnArgHisCysArgGlyAsnGlyPheThrGlyGlyTyrCysThrGlyPheLeu 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION: US-2033116/519A1
GENERAL INFORMATION:
APPLICANT: Decose, Richard
APPLICANT: Eresinner, Georges
APPLICANT: Fregishner, Georges
TITLE OF INVENTION: Chimeric Gene Encoding Drosomycin,
TITLE OF INVENTION: Chimeric Gene Encoding Drosomycin,
TITLE OF INVENTION: Chimeric Containing it and Production of Dise,
TITLE OF INVENTION: Wester Containing it and Production of Dise,
TITLE OF INVENTION: Wester Containing it and Production of Dise,
TITLE OF INVENTION: Wester Containing it and Production of Dise,
FILE REPERENCE: A2889-PCT-USA A-A 072667.0192
CURRENT FELING DATE: 1902-0.11
PRIOR APPLICATION NUMBER: CR97/09,115
PRIOR APPLICATION NUMBER: FR97/09,115
PRIOR APPLICATION NUMBER: FR97/09,663
PRIOR APPLICATION NUMBER: FR97/09,663
PRIOR APPLICATION NUMBER: FR97/09,663
PRIOR PILING DATE: 1997-07-21
PRIOR PILING DATE: 1997-07-21
NUMBER: PASTECE for Windows Version 4.0
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Conservative:
Mismatches:
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Mismatches:
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                                Matches:
Length:
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; ORGANISM: Drosophila melanogaster
US-10-180-247-2
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Best Local Similarity:
Query Match:
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Sequence 2. Application US/10180247

Publication No. US200301675194.

SEMERAL INFORMATION

APPLICANT: DeRose, Richard

APPLICANT: Freysinnet, Georges

APPLICANT: Freysinnet, Georges

APPLICANT: Hoffman, Jules

ITILE OF INVENTION: Chimmeric Gene Encoding Droscmycin,

ITILE OF INVENTION: Transgenic Plants

FILE REFRENCE: A3289-PCT-USA-A-072667.0182

CURRENT APPLICATION NUMBER: US/10/180,247

CURRENT FILING DATE: 2002-06-26

PRIOR APPLICATION NUMBER: PR97/09,115

PRIOR FILING DATE: 1998-07-11

PRIOR FILING DATE: 1997-07-11

PRIOR FILING DATE: 1997-07-14

PRIOR FILING DATE: 1997-07-14
                                  APPLICANT: DeRose, Richard
APPLICANT: DeRose, Richard
APPLICANT: DeRose, Richard
APPLICANT: Freysinnet, Georges
APPLICANT: Hoffman, Jules
APPLICANT: Hoffman, Jules
TITLE OF INVENTION: Chimeric Gene Encoding Droscmycin,
TITLE OF INVENTION: Vector Containing it and Production of Disease-Resistant
TITLE OF INVENTION: Vector Containing it and Production of Disease-Resistant
TITLE OF INVENTION: Vector Containing it and Production of Disease-Resistant
TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: A12889-PCT-USA-A-A 072667.0162
CURRENT FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: PCT/FR98/21462
PRIOR FILING DATE: 1994-07-11
PRIOR APPLICATION NUMBER: FR97/09,115
PRIOR FILING DATE: 1997-07-11
PRIOR APPLICATION NUMBER: FR97/09,163
PRIOR FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 15
SUSTWARE: FASTSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: Ubiquitin drosomycin fusion peptide
US 10 (80)247-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
Indels:
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Matches:
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ORGANISM: Artificial Sequence
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74.50
42.50%
37.50%
22.99%
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Best Local Similarity:
Query Match:
DB:
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Score:
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Sequence 6, Application US/10264480

Sequence 6, Application US/10264480

Squence 6, Application No. US/20030113692A1

GENERAL INFORMATION:
THE CF INVENTION: Inceediu, Bora

TITLE CF INVENTION: FROM THE VENOM OF P. TRANSVAALICUS AND METHODS OF USE
TITLE CF INVENTION: FROM THE VENOM OF P. TRANSVAALICUS AND METHODS OF USE
CURRENT APPLICATION NUMBER: US/10/264,480

CURRENT APPLICATION NUMBER: US/10/264,480

FRIOR FILING DATE: 2002-06-08

PRIOR FILING DATE: 2002-06-08

PRIOR FILING DATE: 2001-0-04

PRIOR APPLICATION NUMBER: 60/327,602

PRIOR FILING DATE: 2001-10-04

NUMBER OF SEQ ID NOS: 33

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 6
                                                                                                                                                                                                                                                                                                 70 AGGASGGGTTACAASGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGCGAG 129
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Publication No. US20030:13892A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hammock, Bruce D.
APPLICANT: Inceeglu, Bora
TITLE OF INVENTION: ISOLATED POLYPEPTIDES AND COMPOSITIONS
TITLE OF INVENTION: FROM THE VENOM OF P. TRANSVAALICUS AND METHODS OF USE
FILE REFERENCE: UCAL256
                                                                                                                                                                                                          13 GGTTCCTGC---GTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGTGAGTGCAAG 69
                                                                                                                                                                                                                                    51 GluGluG.yArgSerSerGlyHisCysSer-----ProSerLeuLysCysTrpCysG.u 68
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-----AsnGluGlyCy8AspLysGluCysLysAlaTyr
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Mismatches:
Indels:
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Mismatches:
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Gaps:
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    Length:
Matches:
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Matches:
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US-10-264-480-6
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LENGTH: 47
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DB:
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Sequence 8, Application US/10264480
Sequence 8, Application OS/10264480
Sequence 8, Application No. US20030113892A1
GENERAL INFORMATION:
APPLICANT: Hammock, Bruce D.
APPLICANT: Inceeglu, Bora
TITLE OF INVENTION: ISOLATED POLYFEPTIDES AND COMPOSITIONS
TITLE OF INVENTION: ISOLATED POLYFEPTIDES AND METHODS OF USE
FILE REFERENCE: UCAL256
CURRENT APPLICATION NOMBER: US/10/264,480
CURRENT APPLICATION NUMBER: 60/393,070
PRIOR APPLICATION NUMBER: 60/393,070
PRIOR APPLICATION NUMBER: 60/393,070
PRIOR APPLICATION NUMBER: 60/327,602
PRIOR FILING DATE: 2001-10-04
NUMBER OF SEO ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 61
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13 SerCysLeuPheGly-----AsnGluGlyCysAspLysGluCysLysAlaTyr 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 GlyGlySerTyrGlyTyrCysTrpThrTrp---GlyGeuAlaCysTrpCysGlu 45
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CURRENT APPLICATION NUMBER: US/10/264,480
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: 60/393,070
PRIOR FILING DATE: 2002-66-28
PRIOR APPLICATION NUMBER: 60/327,602
PRIOR FILING DATE: 2001-10-04
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASTSEQ for Windows Version 4.0
LENGTH: 61
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22.07$
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                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Buthus occitanus
IS-10-264-480-7
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13 GGTTCCTGCGTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGTGAGTGCAAGAGG 72
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GENERAL INFORMATION:
APPLICANT: Navarro Aceved, Pedio A.
APPLICANT: Harvell, Lessie
APPLICANT: Harvell, Reserve
APPLICANT: Harvell, Reserve
APPLICANT: McOutchen, Billy Fred
APPLICANT: McOutchen, Billy Fred
APPLICANT: Worg, James
ITILE OF INVENTION: Defensin Polynucleotides and Methods of
ITILE OF INVENTION: Defensin Polynucleotides and Methods of
ITILE OF INVENTION: Use
ITILE OF INVENTION: Cse
SUPPLIED APPLICATION WINNER: 60/300,152
PRIOR FILING DATE: 2001-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 410, Application US/10178213
Sequence 410, Application US/10178213
Publication No US2030C4:1348A1
GENERAL INFORMATION:
APPLICANT: Simenos, Carl R.
APPLICANT: Harvell, Lesile
APPLICANT: Gohoen, Rebecca
APPLICANT: Herrmann, Rafael
APPLICANT: Hornon, Defensin Polynucleotides and Methods of
ITLE OF INVENTION: Defensin Folynucleotides of
FILE OF INVENTION: USBER: US/12/178,213
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: 6C/300,152
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSEQ for Windows Version 4.3
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Sequence 411, Application US/10178213
Publication No. US20030041348A1
GENERAL INFORMATION:
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Pred. No.:
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46 TCCGATTGCAACGGTGAGTGCAAGAGGGGTTACAAGGGTGGTCACTGCGGTTCCTTC 105
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                                                                                                                                                                                                                                                                                                     42 GlyProCysVal-------SerLysThrAsnCysAlaSerValCysLysThr 56
                                                                                                                                                                                                                                                                                                                                          73 AGGGGTACAAGGGTGCACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGC 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INVESTMENT: CATE R.
APPLICANT: Navarro Acevedo, Pedro A.
APPLICANT: Navarro Acevedo, Pedro A.
APPLICANT: Harvell, Lessie
APPLICANT: Galcoon, Rebecca
APPLICANT: McCutchen, Billy Fred
APPLICANT: Lu, Albert
APPLICANT: Lu, Albert
APPLICANT: Worg, James
TITLE OF INVENTION: Defensin Polynucleotides and Methods of
FILE REFERENCE: 35718/246703
CURRENT APPLICATION NUMBER: 60/300,152
PRICE APPLICATION NUMBER: 60/300,152
PRICE APPLICATION NUMBER: 60/300,241
PRICE FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 387
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Publication No. US20030041348A:
GENERAL INFORMATION:
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) TYPE: PRT

ORGANISM: Glycine max

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TITLE OF INVENTION: AMECAL AND AVINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AMECAL AND AVINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AMECAL MOSA ECR DIAGNOSTICS AND THERAPEUTICS

FILE REPERRICE: 107.96.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PLING DATE: 1998-22-18

PRIOR PLING DATE: 1998-27-18

PRIOR PLING DATE: 1998-27-18
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US-09-252-991A-22334
US-09-252-991A-2666
US-09-252-991A-26657
US-09-252-991A-26657
US-09-252-991A-32162
US-08-415-040-3
US-09-252-991A-32162
US-09-020-216-3
US-09-252-991A-20063
US-09-252-991A-20063
US-09-252-991A-20063
US-09-252-991A-26279
US-09-252-991A-26279
US-09-252-991A-19143
US-09-252-991A-1928
US-09-252-991A-1928
US-09-252-991A-1928
US-09-252-991A-1928
US-09-252-991A-1928
US-09-252-991A-32675
US-09-252-991A-32675
US-09-252-991A-32675
US-09-252-991A-32675
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US-09-252-991A-19400
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US-09-252-991A-19400
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-0=/cgn2 1/USPTO_spool/US09673274/runat 16:02003 170628 2580/app_query.fasta_1.654
-0=Issuede Patente AA -OFMT=fastan -SUFFTx=xi -MINMATCH=0.1 -LOOPCD=0
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-USFEX=US09673274 @CGN 11 SS_@CUNDET 16102003 170628 2580 -NCPUs.6 -ICPU=3
-NO MAXP -LARGEQUERY -NEG SCORES=0 -KAIT -DSPBNCCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Sequence 25, Appl
Sequence 24, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 4, Appli
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26807, A
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Sequence 2, Appli
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849.038 MillIon cell updates/sec
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                                                                                                                                                            October 16, 2003, 17:06:37; Search time 16.8439 Seconds
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                            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                             - protein search, using frame_plus_n2p model
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US-08-435-040-2
US-09-020-210-22
US-09-252-991A-32270
US-08-682-485A-25
US-08-451-472-4
US-08-493-314-25
US-09-400-251-6
US-09-480-251-6
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US-09-251-6
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Maximum Match 100%
Listing first 45 summaries
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, Ygapext
, Fgapext
, Delext
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Perfect score:
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Length:
Matches:
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435.240
FILING DATE: 08-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Slebert, J. Slaanne
REGISTAATION NUMBER: 28,758
REFERENCE/DOCKET NUMBER: 2500.078US2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DCS
                                                      RESULT 3
US-09-020-216-2
; Sequence 2, Application US/39020216
; Parent No. 6:62430
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TELEFAX: (415) 362-5418
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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TOPOLOGY: linear
MOLECULE TYPE: peptide
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ZIP: 94111-4121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity:
48 TrpCys 49
                                                                                                                                                                            GENERAL INFORMATION:
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                                                         200 Argargala-----AlaCysArgGlyGlyLysProArgAspCysGlyCysArgTrpCys 217
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   . . AACCCCTCCTCTTGC . . . . . . . . . ACT 62
                                                                                                                                                                        218 HisArgCysArgArgProGlySerThrAlaSlyProAlaArgAig 232
                                                                                                                         61 CACCGTTGCAATCGGAAGTGTAGTTCACAGCACCCCCACACGCAGG 17
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hammock, Bruce D.
APPLICANT: Herrmann, Rafael
APPLICANT: Moskowitz, Haim
TITLE OF INVENTION: Insect Control With Multiple Toxins
NUMBER OF SEQUENCES: 3
CCRRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: California
COUNTRY: U.S.A.
21P: 94111-4121
COMPUTER FALDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COPENATION SYSTEM: PC-DCS/MS-DCS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/38/435,240
FILLNO DATE: 08-MAY-1995
CLASSIFICATION: 514
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Matches:
Conservative:
Mismatches:
Indels:
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STREET: Four Embarcadero Center, Suite 1450
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NAME: Siedert, J. Suzanie
REGISTRATION NUMBER: 28,758
REFERENCE/DOCKET NUMBER: 2500.078USD
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; Sequence 2, Application US/08435040
; Patent no. 575649
; GENERAL INFORMATION:
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(415) 362-5418
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity:
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Pred. No.:
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STATE: C.
COUNTRY:
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DB:
                                                                                                                                                                                                                                                  RESULT 2
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70 AGGAGGGTTACAAGGGTGGTCACTGC-----GGTTCCTTCGCTAACGTGAACTGC 120
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APPLICANT: Harmock, Bruce D.
APPLICANT: Herrmann, Rafael
APPLICANT: Moskowitz, Hain
APPLICANT: Moskowi
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,216
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Mismatches:
Indels:
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STREET: Four Embardadero Center, Suite 1450
CITY: San Francisc
STATE: California
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117,125
FILING DATE: 24.NOV-1993
ATTORNEY/AGENT INFORMATION:
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55.26%
39.47%
23.61%
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NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                             linear
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APPLICANT:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-451-472-4
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Sequence 32270, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION: WIGHER ALI
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARROGANGS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARROGANGS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169 CCGGATCCGTCGACACGTTCGCCTCGCCGAGCTCTCAAGTCTCGCACCAGCAGTTCACGT 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 TAGCGAAGGAACCGCAGTGACCACCTTGTAACCCCTCCTTGCACTCACCGTTGCAAT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33 ---ArgTyrThrArgAlaProTrpArgCys------CysArgArgArgArg 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 25. Application US/08682485A
Patent No. 5763568
GENERAL INFORMATION:
APPLICANT: ATKINSON, RONALD K
APPLICANT: TYLER, MARGARET I
APPLICANT: TYLER, EDWARD J
TITLE OF INVENTION: Insecticidal Toxins Derived From
TITLE OF INVENTION: Funnel Web (Atrax or Hadronyche Spiders)
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 CGGAAGTGTAGTTCACAGCACCCCACACGCAGGAACCGA 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (S-09-673-274B-2 (1-169) x US-09-252-991A-32270 (1-149)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-OCS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,485A
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/682,485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : Zeneca, Inc.
1200 South 47th Street
                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78.00
49.06%
33.96%
25.74%
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.0607
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Richmond
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ercent Similarity:
est Local Similarity:
nery Match:
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STREET: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             red. No.:
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16 recreserendeserecremenacracracecarrecaacecaacecaacecaacacea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 GGTTACAAGGGTGGTGACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGGTGCGAG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29 GlyGlySerTyrGlyTyrCysTrpThrTrp. - . GlyLeuAlaCysTrpCysGlu 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPESSEE Nixon & Vanderhye PC
STREET: 8th Floor, 1100 No. 5770192th Glebe Road
CITY: Arlington
SIATE: Viginia
COUNTRY: 30A
ZIP: 22201-4714
COMPUTER READABLE POPM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Leiurus quinquestriatus quinquestriatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BIOLOGICAL CONTROL AGENTS 73
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FILING DATE: 17-JULY-1996

PELING DATE: 17-JULY-1996

PILING DATE: 27-JULY-1994

APPLICATION NUMBER: W0 93/15:08

FILING DATE: 29-JAN-1993

APPLICATION NUMBER: M0 93/15:08

FILING DATE: 31-JAN-1992

ATORNEY/AGENT INFORMATION:
NAME: SNAW, Melissa A.
REGISTRATION NUMBER: PFD 5699/D1

REFERENCE/DOCKET NUMBER: PFD 5699/D1

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEGUENCE
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Gaps:
 TELECOMMUNICATION INFORMATION
                 TELEPHONE: $10-231-1542
TELEFAX: $10-231-1312
INFORMATION FOR SEQ 1D NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.127
75.00
51.22%
39.02%
23.15%
                                                                                                                                                                                                                                                                                        0.0812
76.50
55.26%
39.47%
23.61%
                                                                                                                                          MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                          TYPE: amino acid
                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score:
Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
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US-09-403-343B-25
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 G.yGlySerTyrGlyTyrCySTrpThrTrp---GlyLeuAlaCySTrpCysGlu 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: TYLER, MARGARET I
APPLICANT: HOWDEN, MERLIN E.H.
APPLICANT: TYLER, MARGARET I
APPLICANT: TYLER, MARGARET I
TITLE OF INVENTION: Insecticidal Toxins Derived From
TITLE OF INVENTION: Funnel Web (Atrax or Hadronyche Spiders)
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zeneca, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMMITTER READMBLE FORM:

COMPUTER READMBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/933,314
                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
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PRIUS DATE:
PRIOS APPLICATION DATA:
APPLICATION NUMBER: US/08/682,485
FILING DATE: 17-JULY-1996
APPLICATION NUMBER: US/08/256,933
FILING DATE: 27-JULY-1994
APPLICATION NUMBER: WO 93/15108
FILING DATE: 29-JAN-1993
APPLICATION NUMBER: AU PLO722
FILING DATE: 31-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: SABA, MAISSA A
REGISTRATION NUMBER: 38,301
REGISTRATION NUMBER: 38,301
                                                                                                                                                                                                                                                                                                                                                                    Gaps:
REGISTRATION NUMBER: 32,955
REFRENCE/COCKET NUMBER: 117-187
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816 4000
TELEFAX: (703) 816 4100
TELERSAX: (703) 816 4100
TELERSAX: NIXN UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 61 armic acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Zeneca, Inc.
1200 South 47th Street
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; Sequence 25, Application US/08933314
: Patent No. 5959182
                                                                                                                                                                                                                                                                                            76.50
55.26%
39.47%
23.61%
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CITY: Richmond
STATE: California
                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                  TCPOLOGY:
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Pred. No.:
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Sequence 25. Application US/09403343B

Patent No. 655501

GRNERAL INFORMATION:
APPLICANT: JOLIVET-REYNAUD, COLETTE
APPLICANT: DIVET-REYNAUD, COLETTE
APPLICANT: DIVET-REYNAUD, COLETTE
APPLICANT: PERRON, HERVE
TITLE OF INVENTION: POLYPEPTIDE CAPABLE OF REACTING WITH ANTIBODIES OF
TITLE OF INVENTION: PATIENTS SUFFERING FROM MULTIPLE SCLEROSIS AND USES
FILE REFERENCE: 104574
CURRENT APPLICATION NUMBER: ER/97/05679
FRIOR APPLICATION NUMBER: ER/97/05679
PRIOR APPLICATION NUMBER: FR/97/16870
PRIOR FILING DATE: 1997-04-29
PRIOR FILING DATE: 1997-04-29
PRIOR FILING DATE: 1998-04-29
PRIOR FILING DATE: 1998-04-29
PRIOR FILING DATE: 1998-04-29
SPRIOR FILING DATE: 1998-04-29
SPRIOR FILING DATE: 1998-04-29
NUMBER OF SEQ ID NOS: 34
SEQ ID NO S: 34
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                                                                                                                                                                                                                                                                                                                                                            16 TCCTGCGTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGTGAGTGCAAGAGAGGAGG 75
                                                                                                                                                                                                                                                                                                                                                                                             76 GGTTACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGCGAG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 GlyGlySerTyrGlyTyrCysTrpThrTrp---GlyLeuAlaCysTrpCysGlu 45
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ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Leiurus quinquestriatus quinquestriatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 4 5 6 4 6
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12
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
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                                                                                                                                                                                                                   Mismatches:
Indels:
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Alignment Scores:
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Pred. No.:
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                                                                                                                                                                   Sequence 4, Application US/09480251

Patent No. 6465719

GENERAL INFORMATION:
APPLICANT: DeRose, Richard
APPLICANT: Freyssinet, Georges
APPLICANT: Hoffman, Unles
TITLE OF INVENTION: Chimeric Gene Encoding Drosomycin,
TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: A32889-PCT-USA-A
FILE REFERENCE: PCT-USA-A
CURRENT APPLICATION NUMBER: BCT/FR98/01462
PRIOR FILING DATE: 1998-07-08
PRIOR FILING DATE: 1998-07-08
PRIOR FILING DATE: 1999-07-01
PRIOR FILING DATE: 1997-07-11
PRIOR FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 4
LENGTH: 44
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Patent No. 6465719
GENERAL INFORMATION:
APPLICANT: Preyssinet, Georges
APPLICANT: Freyssinet, Georges
APPLICANT: Hoffman, Jules
TITLE OF INVENTION: Chimeric Gene Encoding Drosomycin,
TITLE OF INVENTION: Transgenic Plants
FILE REFERENCE: A32889-FCT-USA-A
FILE REFERENCE: 2000-01-11
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 1998-07-08
PRIOR APPLICATION NUMBER: FRANCE 97/09,115
PRIOR FILING DATE: 1997-07-11
106 GCTAACGTGAACTGCTGCTGCGAGACTTGAGAGCTCGGCGAGGCGAACGTGTCGACGGAT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 AGGAGGGTTACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGCGAG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 GluGluGlyArgSerSerGlyHisCysSer-----ProSerLeuLysCysTrpCysGlu 42
                          40 SerGlyLeuAlaCysTrpCysAsn-----AspLeuProGluAsnValProlleLysAsp 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 GGTTCCTGC---GTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGCTGAGTGCAAG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 GlyProCysAlaValTrpAsp------AsnGluThrCysArgArgValCysLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IS-09-673-274B-2 (1-169) x US-09-480-251-4 (1-44)
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Drosophila melanogaster
35-09-480-251-4
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74.50
42.50
37.50
22.99
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Percent Similarity;
Percent Similarity;
Percent Match:
                                                                      166 CCG 168
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APPLICANT: Defice, Richard
APPLICANT: Freyssinet, Georges
APPLICANT: Freyssinet, Georges
APPLICANT: Freyssinet, Georges
APPLICANT: Freyssinet, Georges
APPLICANT: Hoffman, Jules
ITILE OF INVENTION: Chimeric Gene Encoding Drosomycin,
ITILE OF INVENTION: Transgenic Plants
ITILE OF INVENTION: Transgenic Plants
FILE REFERENCE: A12889-PCT-UGA-A
CURRENT FILING DATE: 1090-01-11
PRIOR FILING DATE: 1998-07-08
PRIOR FILING DATE: 1998-07-08
PRIOR FILING DATE: 1997-07-11
PRIOR PLING DATE: 1997-07-14
PRIOR FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FRANCE 9709,663
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FRANCE 9709,663
SOFTWARE: FRANCE 9709,663
SOFTWARE: FRANCE 9709,663
SOFTWARE: FRANCE 9709-115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 AGGAGGGTTACAAGGSTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGCGAG 129
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OTHER INFORMATION: The ubiquitin - drosomycin fusion peptide
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                                                                            FastSEQ for Windows Version 3.0
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; Sequence 2, Application US/09480251
; Patent No. 6465719
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US-09-480-251-2
PRIOR APPLICATION NUMBER: FRAN,
PRIOR FILING DATE: 1937-07-24
) NUMBER OF SEQ 1D NOS: 15
SOTUMARE: FASTSEQ for Windows: SEQ 1D NO 6
| LENGTH: 69
| TYPE: PRT
| ORGANISM: Artificial Sequence
                            1997-07-24
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Best Local Similarity:
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUMBER: US 090252,991A
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING LOAD: 1998-02-18
PRIOR FILING DATE: 1998-02-18
FILING APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
TITLE CP INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS:
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/99/252,991A
CURRENT FILING DATE: 1999-02-18
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                                                                                                                                                                           163 CCGTCGACACGTTCGCCTCGCCGAGCTCTCAAGTCT-----CGCACCAGCAGTTCACGT 110
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                                                                                                                 US-09-673-274B-2 (1-169) x US-09-252-991A-22334 (1-145)
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; Patent No. 6551795
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US-09-252-991A-26857
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Pred. No.:
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Sequence 22314. Application US/09252991A
Sequence 22314. Application US/09252991A
Sequence 22314. Application US/09252991A
SEQUENCEST INFORMATION:
APPLICAMY: Marc J. Rubenfield et al.
APPLICAMY: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-27
NUMBER: US 60/094,:90
PRIOR PILING DATE: 1998-07-27
NUMBER: US 62334
SEQ ID NOS: 33142
                                                                                                                                                                                             PARCEAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE DE INFORMATION:
TITLE DE INVENTION: NUCLEIC ACID AND AMINO ACID SEGUENCES RELATING TO PSEUDCMONAS
TITLE DE INVENTION: AREUGINCSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33:42
SEQ ID NOS: 33:42
SEQ ID NOS: BEG ID NOS: ASSETT OF TABLE OF
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26 ProSerProAlaThrArgLysProArg-----SerProSerAlaSerAlaArg 41
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Matches:
                                                                                                                                         Sequence 26837, Application US/09252991A
Patent No. 6551795
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ORGANISM: Pseudomonas aeruginosa
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US-09-252-991A-22334
                                                                                           RESULT 12
US-09-252-991A-26807
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Length: 397
Matches: 20
Conservative: 5
Mismatches: 23
Indels: 0
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26857
LENGTH: 397
TYPE: PRT
ORGANISM: Reeudomonas aeruginosa
S-09-252-991A-26857
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q	270 PrcSerArgSe		68
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Q	290 ArgArgArgSe	290 ArgArgArgSerSerSerGlyArgSerThrProSerTrpCysThrArg-ValAlall 309	60
≿	49 CGGAAGTGTAG	49 CGGAAGTGTACATCACACCCCA 25	
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S-09-673-274B-2 (1-169) x US-09-252-991A-26857 (1-397)

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C)Accession: A29386
R; Vargas, O; Martin, M.F.; Rochat, H.
R; Vargas, O; Martin, M.F.; Rochat, H.
Eur. J. Blochem 162, 589-599, 1987
A; Title: Characterization of six toxins from the venom of the Moroccan scorpion Buthus
A; Title: Characterization of six toxins from the venom of the Moroccan
A; Reference number: A29386; MUD: 87161829; PMID: 3104036
A; Molecule type: protein
A; Molecule type: protein
A; Readules: 1-66 vVMR.
C; Superfamily: scorpion neurotoxin
C; Keywords: neurotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 GGTTACAAGGGTGGTCACTGCGGTTCCTTC----GCTAACGTGAACTGCTGGTGCGAG 129
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depressant insect
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C,Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 07-Feb-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neurotoxin X - scorpion (Leiurus quinquestriatus)
C;Species: Leiurus quinquestriatus hebraeus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neurotoxin III - scorpion (Buthus occitanus)
                                                                                                                                                        NTSR12
JN0669
JN0669
JN08612
JN08679
J
JN0670
NTSR2N
D59352
NTSR9E
NTSR1A
NTSR5M
                                                                                                                       B59352
C59352
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Pred. No.:
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DB:
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##MODEL=frame+n27-model - DEV=x1p

- DB=PIR 76 - QPMT=fastan - SUPFIX=Tpr - MINMATCH=0.1 - LOOPCL=0 - LOOPEXT=0

- DG=PIR 76 - QPMT=fastan - SUPFIX=Tpr - MINMATCH=0.1 - LOOPCL=0 - LOOPEXT=0

- DOCALIGN=200 - THR SCORE=pcr - THR MAX=100 - TRR MINGN=0 - ALIGN=15 - MCDE=LOCAL

- DOCALIGN=200 - THR SCORE=pcr - THR MAX=100 - TRR MINEN=0 - MAILGN=15 - MCDE=LOCAL

- OUTFWT=ptc - NORM=ext - HEAPSIZE=550 - MINLEN=0 - MAXLEN=2000000000

- USR=uCNO9673274 @CGN 1 1 77 @runat 16102003 170628 2555 - NCPU=6 - ICPU=3

- NO MADP - LARGEQUERY - NEG SCOREESO - WAIT - DSPBLOCK=100 - LONGLOG

- DEV TIMEOUT=120 - WARN TIMEOUT=30 - THREADS=1 - XGARPEXT=0.5 - FGAPOP=6

- FGAPEXT=7 - YGAPEXT=0 - YGAPEXT=0.5 - DELOP=6 - DELEXT=7
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V-5 - b
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neurotoxin IV - Eg
depressant insect
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neurotoxin X - sco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neurotoxin M14 - 1
neurotoxin 1 - bar
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neurotoxin V - Egy
neurotoxin 3 - bar
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                                                                                                                                           (without alignments)
1564.690 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                       October 16, 2003, 17:06:37; Search time 16.2259 Seconds
                                                                                                                                                                                                                                gataagcttatcggttcctg......tgaactgctggtgcgagact 132
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                      - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                       hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                        283308 segs, 96168682 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                             US-09-673-274B-2_COPY_1_132
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A59222
A55869
S68906
NTSR41
B34123
NTSR4C
A55824
C23727
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NTSR5L
NTSR3C
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, Ygapext
, Fgapext
, Delext
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Match Length
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Ygapop 10.0
Fgapop 6.0
Delop 6.0
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1: pir1:*
2: pir2:*
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4: pir4:*
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Result Š ~

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A; Experimental source: clone pcD-634
R; Kopeyan, C.; Martinez, G.; Rochat, H.
Eur. J. Biochem. 94, 609-615, 1979
A; Title: Amino acid sequence of neurotoxin III of the scorpion Androctonus australis F
A; Reference number: A01740; MUID:79148414; PMID:428402
A; Accession: A01740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NyAlternate names: mammalian neurocoxin II
C;Species: Androctonus australis (Sahara scorpion)
C;Date: 30-59-1979 #sequence_revision 04-0ct-1996 #text_change 18-Jun-1999
C;Accession: C34444; Ac1740
R;Bougis, P.E.; Rochat, H.; Smith, L.A.
J. Biol, Chem. 264, 19259-19255, 1998
A;Title: Precursors of Androctonus australis scorpion neurotoxins. Structures of precu
                                                                                             C;Species: Buthus occitanus tunetanus
C;Date: 23.-011-1997 #sequence_revision 01-Aug-1997 #text_change 16-Jul-1999
C;Accession: 588906
R;Bouhaouala-Zahar, B.; Ducarcel, F.; Zenouaki, I.; ben Khalifa, R.; Borchani, L.; Pel
Eur. J. Blochem. 238, 553-660, 1996
A;Tile: A recombinant insect-specific alpha-toxin of Buthus occitanus tunetanus scorp
A;Reference number: 568906; MUID:96300228; PMID:8706664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-84 <BOU>
A;Cross-references: GB:M27703; GB:J05102; NID:g161142; PIDN:AAA29948.1; PID:g161143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76 GGTTACAASGGTGGTCACTGCGGT-----TCCTTCGCTAACGTGAACTGCTGGTGCGAG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 TCCTGCGTCTGGGGTGCTGTGACTACACTTCCGATTGCAACGGTGAGGGCAAGAGGAGGAGG 75
                                                                                                                                                                                                                                                                                                               A;Accession: 568906
A;Status: preliminary
A;Otatus: preliminary
A;Roidecule type: mRNA
A;Cross-references: GB:X92376; NID:g1041277; PIDN:CAA63120.1; PID:g1041278
C;Superfamily: scorpion neurotoxin
F;1-18/Domain: signal sequence #status predicted <SIG>F;19-85/Product: alpha-toxin #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F.1-19/Domain: signal sequence #status predicted <SIG>
F.20-83/Product: neurotoxin III #status experimental <MAT>
F.31-81,35-53,39-63,43-65/Disulfide bonds: #status predicted
                                                                  Bot XIV precursor - scorpion (Buthus occitanus)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85
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Mismatches:
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Mismatches:
Indels:
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Matches:
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Matches:
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A; Residues: 20-26, 'N', 28-83% KOP
C; Superfamily: scorpion neurotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.50
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29.40
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79.00
50.00%
35.00%
29.59%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
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Pred. No.:
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                                                                         alpha-toxin
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Crustacean specific toxin : - scorpion (Centruroides limpidus)
C; Species: Centruroides limpidus limpidus |
C; Species: Centruroides limpidus |
C; Species: Circle |
C; Specie
                                                                                                                                        new scorpion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 AGGAGGGTTACAAGGGTGGTCACTGC------GGTTCCTTCGCTAACGTGAACTGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 TCCTGCGTGTGG-----GGTGCTGTGAACTACACTTCCGATTGCAACGGTGAGTGCAAG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.2 AshCysValTyrThrCysGlyAlaAshSerTyr·······CysAshThrGluCysChr 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 LysaksndiyAlaGluSerGlyTyrCysGlnTrpPheGlyLysTyrGlyAsnAla---Cys 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19 TGCGTGTGGGGGGGGGAACTACACTTCCSATTGCAACGGTGAGTGCAAGAGGAGGGGT 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 CysPheTrpLeuGlyLysAsn----GluAsnCysAspLysGluCysLysAlaLysAsn 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 TACAAGGGT-----GGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGCGAG 129
C)Date: 31 Dec-2001 #sequence_revision 31-Dec-2001 #text_change 19-Apr-2002 C)Accession: A59222
R)Corzo, G : Escoubas, P.; Nakajima, T. submitted to the Protein Sequence Database, April 2000
A)Description: A procedure for the rapid purification of non commercial and A)Reference number: A5922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 GinGlyGlySerTyrGlyTyrCysTyrSerPheAla------CysTrpCysGlu 49
                                                                                                                                                                                                                                                                                                                               C.Superfamily: scorpion neurotoxin

?/Reywords: amidated carboxyl end; neurotoxin; venom

F.13.64.17.37.20-47.27-49/Disulfide bonds: #status predicted

F.65/Modified site: amidated carboxyl end (Arg) #status predicted
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Matches:
Conservative:
Mismatches:
Indels:
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Mismatches:
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79.50
53.85%
43.59%
29.78%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.117
80.50
57.14%
40.48%
                                                                                                                                                                                                                                  A Status: preliminary
A Molecule type: protein
A Residues: 1-65 <COR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 TGGTGC 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
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Rest Local Similarity:
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Cipecies: Mesoburhus eupeus (Jesser Asian scorpton)
Cipate: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 31-Dec-1993
Aritle: Study of neurotoxins from the venom of central Asian scorpion Buthus eupeus.
Arecession: JT322
Aritle: Study of neurotoxins from the venom of central Asian scorpion Buthus eupeus.
Arecession: JT322
Arecession: JT322
Arecession: JT322
Cicament: The venom of this scorpion contains three major polypeptide neurotoxins: M9, Cicament: The venom of this scorpion neurotoxin
Cirament: The venom neurotoxin
Cirament: Arecession: Venom
Cirament: Arecession: Venom
Cirament: Arecession: Venom
                    A,Title: Functional duality and structural uniqueness of depressant insect selective: A,Reference number: A38526; MUD:91230120; PMID:2029523
A,Accession: B38526
A,Molecule type: protein
A,Residues: 1-61 < ZLO2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 TGCAACGGTGAGTGCAAGAGGAGGGTTACAAGGGTGGTCACTGC------GGTTCC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.
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C;Species: Centruroides sculpturatus (bark scorpion)
C;Decies: 22-Jun-1981 #sequence_revision 22-Jun-1981 #text_change 31 Mar 2003
C;Accesaion: A01725
C;Accesaion: A01725
Arch. Biochem. Biophys. 164, 694-706, 1974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 TCCTGCGTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGTGAGTGCAAGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---AsnGluGlyCysAsnLysGluCysLysSerTyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diyalySerTyralyTyraysTpThrTrp---GlyLeuAlacysTrpCysGl: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               76 GGTTACAASGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGCGAG
                                                                                                                                                                                                                                                                                           F;10-60,14-35,21-42,25-44/Disulfide bonds: #status predicted
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113
8 4 4 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neurotoxin Mi4 - lesser Asian scorpion
                                                                                                                                                                                       A)Cross-references: CAS::33300-67 3
C,Superfamily: scorpion neurotoxin
C,Keywords: neurotoxin; venom
1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.418
76.00
59.62%
44.83%
28.46%
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76.50
55.26%
29.47%
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iochemistry 30, 4814-4821,
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Best Local Similarity:
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NTSR1C
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4,Rosaidues: 1-61 «ZLO1»
3,Kopeyan, C.; Mansuelle, P.; Sampieri, F.; Brando, T.; Bahracui, E.M.; Rochat, H.; Gran
728S Lett. 261, 423-426, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   venom of Lei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              iyMolecule type: protein
1,Residues: 1-61 <KOP>
1,Zlotkin, E.; Eitan, M.; Bindokas, V.P.; Adams, M.E.; Moyer, M.; Burkhart, W.; Fowler,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leiurus quinquestriatus quinquestriatus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 AGGAGGGGTTACAAGGGTGGTCACTGC-----GGTTCCTTCGCTAACGTGAACTGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 AsnCysValTyrThrCysGlySerAsnSerTyr-----CysAsnThrGluCysThr 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 LysAsnGlyAlaGluSerGlyTyrCysGlnTrpLeuGlyLysTyrGLyAsnAla---Cys 47
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                                                                                                    75
                                                                                                                                                               30 AsnCysValTyrHisCysVal-----ProProCysAspGlyLeuCysLysLysAsn 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               **Species: Leiurus quinquestriatus quinquestriatus)

**Species: Leiurus quinquestriatus quinquestriatus

***Species: Leiurus quinquestriatus quinquestriatus

***Species: Leiurus quinquestriatus quinquestriatus

****Species: Leiurus quinquestriatus quinquestriatus

****Species: Leiurus quinquestriatus quinquestriatus

*****Species: Leiurus quinquestriatus quinquest
                                                                                                                                                                                                                                                                                                                                                                                                                           reurotoxin IV - Egyptian scorpion
;/species: Leiurus quinquestriatus (Egyptian scorpion)
;/bate: 15-0ct-1982 #sequence_revision 27-Nov-1985 #text_change 28-Aug-1998
;/Accession: A01749
;/Kopeyan, C.; Martinez, G.; Rochat, H.
;/Kopeyan, C.; Martinez, G.; Rochat, H.
;/Title: Primary structure of toxin IV of Leiurus quinquestriatus quinquestri
;/Reference number: A01749
                                                                                                                                                                                                                             76 GGTTACAAGGGTGGTCACTGCGGTTCCTTC-----GCTAACGTGAACTGCTGGTGC 126
                                                                                                TCCTGCGTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGTGAGTGCAAGAGGAGG
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                               S-09-673-274B-2_COPY_1_132 (1-132) x NTSR3A (1-84)
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77.50
57.14%
38.10%
29.03%
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Best Local Similarity:
Query Match:
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C.Species: Leiurus quinquestriatus (Egyptian scorpion)
C.Species: Leiurus quinquestriatus (Egyptian scorpion)
C.Date: 30-Apr.1979 #sequence_revision 13-Jul-1981 #text_change 15-Oct-1996
C.Accession: A0174:
R.Kopeyan, C.; Martinez, G.; Rochat, H.
FBBS Lett. 89, 54-58, 1978
A;Title: Amino acid sequence of neurotoxin V from the scorpion Leiurus quinquestriatu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neurocoxin IV - Sahara scorpion
C;Species: Androctorus australis (Sahara scorpion)
C;Date: 30-1993 #sequence_revision 3C-Sep-1993 #text_change 07-May-1999
C;Accession: 3C1321
R;Mansuelle, P.; Martin, M.F.; Rochat, H.; Granier, C.
Natural Toxins: 1, 61-69, 1992.
A;Title: The amino acid sequence of toxin IV from the Androctonus australis scorpion:
A;Reference number: CC1321; MUID:94221398; PMID:1344902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 SerCysVal ------AlaAsnAsnTyr ------Cy9AspAsnGlnCysLy9MetLy9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 TCTGCGTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGTGAGTGCAAGAGGAGG
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C;Accession: C23727
R;David, R.M.; Krishna, N.R.; Watt, D.D.
Toxicon 29, 645-65, 1991
A;Title: Characterization of cattonic binding sites of neur
A;Reference number: A23727; MUID:92023284; PMID:1926166
A;Reference number: A23727; MUID:92023284; PMID:1926166
A;Reference protein
A;Residues preliminary
A;Molecule type: protein
A;Residues: 1-59 < ADAv>
C;Superfamily: scorpion neurotoxin
C;Keywords: neurotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches:
Conservative:
Mismatches:
Indels:
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A;Residues: 1.64 «MAN»
C.Superfamily: scorpion neurotoxin
C;Keywords: neurotoxin
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74.00
59.26%
44.44%
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74.00
60.53$
42.11$
27.72$
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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Pred. No.:
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   A;Tille: Amino acid sequences of neurotoxic protein variants from the venom of Centrurol A;Reference number: A9058; MUID:75163395; PMID:4460885
A;Accession: A01752
A;Accession: A01752
A;Molecule type: protein
A;Residues: i-65 - BAB>
C;Superfamily: scorpion neurotoxin
C;Keywords: neurotoxin; venom
F;12-64;16-41,27-46,29-48/D;sulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Groscowyth precursor - fruit fly (Drosophila melanogaster)

NyAlternate names: cysteine-rich peptide

C.Species Lorsophila melanogaster

C.Species Lorsophila melanogaster

C.Species Lorsophila melanogaster

C.Accession: A55824; 838575

C.Accession: A55824; 838575

C.Accession: A55824; 838575

C.Accession: A55824; 838575

C.Accession: A55824; Billet, P. Michaut, L.; Lagueux, M.; Broekaert, W.F.; Herru, C.; Hoffman A, Title: Insect immunity. Septic anjury of Drosophila induces the synthesis of a potent A, Reference number: A55824; MUD:95105209; PMID:7806546

A.Reference number: A55824; MUD:95105209; PMID:7806546

A.Residues: L.70 - FEH.

A.Residues: L.70 - FEH.

A.Rocossion: A55824

A.Rocossion:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 CyspheTrpLeuGlyLysAsnGluHlsAsnThiCysGluCysLysAlaLysAsnGlnGly 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neurotoxin V-5 - bark scorpion
C/Species: (entruroides sculpturatus (bark scorpion)
C/Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 07-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGTTCCTGC - - - GTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGTGAGTGCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65
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15
13
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A)Gene. FlyBase:Drs
A,Cross-references: FlyBase:FBgnC010381
C)Keywcros: disultate bond, extracellular protein
E)27-70/Product: drosomycin #status experimental <MAT>
                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
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37.50%
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75.50
51.358
37.84$
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424624

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Astronomical source: Various course to the text change 16 cul. 1999
C.Species: Centrutoides noxius
C.Species: Centrutoides noxius
C.Accession: Mo670
R.Becerrii, B.; Vazquez, A.; Garcia, C.; Corona, M.; Bolivar, F.; Fossan;, L.D.
Gene 128, 165-171, 1993
A:Title: Cloning and characterization of cDNAs that code for Na*-channel blocking form A; Reference number: JN0679
M:Rosidues: 1-87
A; Rosidues: 1-87
A; Coss references: GB:L05061; KID:g304569; PIDN:AAA28286:1; PID:q304569
A; Rosidues: 10-87
A; Coss references: GB:L05061; KID:g304569; PIDN:AAA28286:1; PID:q304569
A; Rosidues: 1-87
A; Coss references: CB:L05061; KID:g304569; PIDN:AAA28286:1; PID:q304569
A; Rosidues: 1-87
A; Coss references: GB:L05061; KID:g304569; PIDN:AAA28286:1; PID:q304569
A; Rosidues: 1-87
A; Coss references: GB:L05061; KID:g304569; PIDN:AAA28286:1; PID:q304569
A; Rosidues: 1-87
A; Coss references: GB:L05061; KID:g304569; PIDN:AAA28286:1; PID:q304569
A; Rosidues: 1-87
A; Coss references: GB:L05061; KID:g304569; PIDN:AAA28286:1; PID:q304569
A; Rosidues: 1-87
A; Coss references: GB:L05061; KID:g304569; PIDN:AAA28286:1; PID:q304569
A; Rosidues: 1-87
A; Coss references: GB:L05061; KID:g304569; PIDN:AAA28286:1; PID:q304569
A; Rosidues: 1-87
A; Coss references: GB:L05061; KID:g304569; PIDN:AAA28286:1; PID:q304569
A; Coss references: GB:L05061; KID:g304569; PID:g304569:1; PID:g304569
A; Coss references: GB:L05061; KID:g304569; PIDN:ga:L05061; PID:g304569; PID:g304569; PID:g304569]
A; Coss references: GB:L05061; KID:g304569; PIDN:ga:L05061; PID:g304569; PID:g304699; PID:g3
                                                                                                                                                                                                                                            JNC670
Na+-channel-blocking texin (clone engill) precursor - scorpion (Centruroides nexius)
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             32 LysAsnGlnGlyGlySerTyrGlyTyrCysTyrAlaPheAla-----CysTrpCys
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Ne : 17.2259 secs
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38.46%
26.40%
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Species: Centruroides sculpturatus (bark scorpion)

Species: Centruroides sculpturatus (bark scorpion)

Species: Sect. 1982 #sequence revision i5-Oct.1982 #text_change 23.Aug.1996

Accession: A90058; A94470; A01754

Rababin, D.R.: Watt, D.D.; Goos, S.M.; Mlejnek, R.V.

Arch. Biochem Biophys. 164, 694-706, 1974

Arthile: Amino acid sequences of neurotoxic protein variants from the venom of Centruroi A; Reference number: A90058; MUID:75163395; PMID:4460885
A, Neference number: A01741; MUID:78191225; PMID:658402
A,Note: L. q. quinquestriatus
A,Accession: A01741
A,Molecule type: protein
A;Residues: 1-64 <KOP>
S;Superfamily: scorpion neurotoxin
C;Keywords: blocked carboxyl end; neurotoxin; venom
F;12-63,16-36,22-46,26-48/Disulfide bonds: #status predicted
F;12-63,16-36,22-46,26-48/Disulfide bonds: #status predicted
F;12-64,Modified site: blocked carboxyl end (Asn) (propably amidated) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1-7, 1982
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A.Reference number: A94314; MUID:82200153; PMID:7080025
A.Contents: annotation; X-ray crystallography, 1.8 angstroms; disulfide bonds
A:Note: X-ray crystallographic studies were based on the revised sequence shown
C:Superfamily: scorpion neurotoxin
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A;Residues: 1-65 < BHO>
4;Fontecilla-Camps, J.C.; Almassy, R.J.; Suddath, F.L.; Bugg, C.E.
Toxicon 20, 1-7, 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2;Keywords: neurotoxin; venom
5;12-65,16-41,25-46,29-48/Disulfide bonds: #status experimental
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A;Residues: 1-24, 'NTC', 28-63, 'CS' <BAB>
A;Bhown, A.; Mole.
J.
Inpublished results, cited by Fontecilla-Camps, J.C., et
A;Reference number: A94470
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Mismatches:
Indels:
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73.00
60.71$
42.86$
27.34$
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36.59%
26.40%
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Q9gua7 mesobuthus
Q9vz13 drosophila
Q95p69 mesobuthus
Q9fpg1 phaseolus a
Q9u6u0 mytilus gai
                                                                                                                                                                    Q9y0a9 mytilus gal
Q8ird6 drosophila
Q9vzq4 drosophila
Q9y0b mesobuthus
Q39401 brassica ca
Q8whsz mus musoulu
                                                                                                                                                                                                                                                                                                                         29blmc androctonus
P82762 arabidopsis
Q8ird7 drosophia
                        09xy87 mesobuthus
Q8t3t0 mesobuthus
P82761 arabidopsis
                                                                                                                                                                                                                                     P91904 caenorhabdi
076963 crthochirus
099h52 nectria rad
                                                                                                                                                                                                                                                                            Q9whf2 agrotis seg
Q26292 leiurus qui
                                                                                                                                                                                                                                                                                             P82759 arabidopsis
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                                                                                                                                                                                                                                                                                                                QBaxp0 cynops pyrr
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O945d8 castanea sa
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                                                                               09vzr2 drosophila
08wry4 centruroide
09gua7 mesobuthus
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                                                              Q8mvs7 leturus qui
                                                                                                                                                                                                                              Q9twil centruroide
       mesobuthus
mesobuthus
                                                     Q9vzq5 droscphila
                                                                     O9ylu3 mesobuthus
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                                                                                                                                                            Q8mvs8 leiurus
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Eukaryota: Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea: Buthidae; Mescbuthus.
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281RD7
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P8276;
09VZ05
09Y1U3
09VZR2
09WZY4
09GUA7
09GUA7
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Q85MD9
Q8AXP0
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Q8RCM0
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Q8VHS2
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                                                                                                                               Q9FPG1
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C8IRD6
09VZC4
C9Y0B8
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08MVS8
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NCBI_TaxID=34649;
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**MODEL=frame+ n2p.model -DEV=xlp
-MODEL=frame+ n2p.model -DEV=xlp
-O=/cgn2 1/108TO spool/US09673274/runat 16102003 170627 2545/app query.fasta_1.654
-DB=SPTREMBL_23 -QFMT=fastan -SUFFIX=rspt -MINMATCH=0.1"-LOOPCL=0 -LOOPEXT=0
-DB=SPTREMBL_23 -QFMT=fastan -SUFFIX=rspt -MINMATCH=0.1"-LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=bits -TRANS=human40.cdi -LiGT=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXIZEN=200000000
-USER=US09673274_@CGN 1 1 216 @runat 16102003 170627 2545 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=20 -XGAPEXT=7.
                                                             October 16, 2003, 17:06:37 ; Search time 39.0299 Seconds (without alignments) 1745.479 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q17231 mesobuthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                       gataagcttatcggttcctg......tgaactgctggtgcgagact 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description
        GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                             - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                  otal number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
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Buthoidea, Buthidae, Mesobuthus
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Mesobuthus martensii (Manchurian scorpion) (Buthus martensii).
Scorpi
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7317 MW; ECDCC391B733EC0A CRC64;
                                                                                                                                                                                                      7285 MW; F13FCD7153855626 CRC64;
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InterPro, IPR001219; Neurotoxin.
InterPro; IPR002061; Scorpion_toxini.
Pfam; PF00537; toxin 3; 1.
PRINTS; PR00264; TOXIN.
ProDom; PD000908; Scorpion_toxinl; 1.
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01-NVV-1996 (TrEMBLrel. 01, Created)
01-NVV-1996 (TrEMBLrel. 01, Last seq
01-NAR-2003 (TrEMBLrel. 23, Last and
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SEQUENCE 65 AA; 7285
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RESULT C17230

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Wang C., Ling M., Wang D., Chi C.;

"The gene for depressant insect toxin BmK ITb from Chinese scorpion, Buthus marrensia Karsch.";

Buthus marrensia Karsch.";

Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

C. !- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).

C. !- SIMILARITY BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.

REMBL, AF272777; AAF77063.2;

RINGERPO; IPR003614; Knot1.

REMBL, AF272777; AAF77063.2;

RINGERPO; IPR003614; Knot1.

REMBL, SOURCEOST, LOCATION.

REMBL, SOURCEOST, COXIN. 1.

REMBL, SOURCEOST, COXIN. 1.

REMBL, SOURCEOST, COXIN. 1.

REMBL, SAMART, SMC505; Knot1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 SerCysLeuTrpG.y-----AsnGluGlyCysAsnLysGluCysLysGlyPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annocation update)
Depressant insect neurotoxin BmK ITb precursor.
Mesobuthus martensii (Marchurian scorpion) (Buthue martensii).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Butholdea; Buthidae; Mesobuthus.
                                                                                                                                                                                                                                                                                                                                                                                           Mesobuthus martensii (Manchurian scorpion) (Buthus martensii).
Eukarycta; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Mesobuthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 GGTTACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGCGGAG 129
76 GGTTACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGCTGCGGAG 129
                                                             46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        an
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MEDLINE=22217668; Pubxed=122330558;
Peng F., Zeng X.C., He X.H., Pu J., Li W.X., Zhu Z.H., Liu H.;
Peng F., Zeng X.C., He X.H., Pu J., Li W.X., Zhu Z.H., Liu H.;
"Molecular cloning and functional expression of a gene encoding antiarrhythmia peptide derived from the scorpion toxin.";
Eur. J. Blochem. 269:4468-4475(2002).

EMBL, AF459791; AANS9782.1;
EMBL, AF459791; AANS9782.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9425 MW; 5076039B9966AA6F CRC64;
                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Depressant scorpion toxin KIM2 precursor.
KIM2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches:
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score:

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PRELIMINARY;
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RESULT 6
Q8T3T0
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DB:

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Hypothetical protein LCR46 precursor.
LCR46.
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92:4 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80.50
52.63$
39.47$
30.15$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pland TAC clones.";
DNA Res. 6:183-195(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00505; Knot1;
Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . A.
                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity:
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IDENTIFICATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
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P82761
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                                                                                                                                                                                                                                                                                                                                   16 TCCTGCGTGTGGGGTGCTGTGAACTACACTTCCGATTSCAACGGTGAGTGCAAGAGGAGG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCCTGCGTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGTGAGTGCAAGAGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 SerCysLeuTrpGly-----AsnGluGlyCysAsnLysGluCysArgAlaTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel, 12, Created)
01-NOV-1999 (TrEMBLrel, 12, Last sequence update)
01-NOV-1999 (TrEMBLrel, 13, Last annotation update)
Neurotoxin AEP precursor.
Mescobuthus martensi (Manchurian scorpion) (Buthus martensii).
Bukaryota, Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones; Buthoidea; Buthoidea; Mesobuthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGTTACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGCGGAG 129
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                                                                                                                                                                                                                                                                                                                                                                                                                              50 GlyAlaTyrTyrGlyTyrCysTrpThrTrp---GlyLeuAlaCysTrpCysGln 66
                            DEPRESSANT INSECT NEUROTOXIN BMK ITB 80CDD3914956DE8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ling M.H., Wang C.G., Wang D.C., Ch. C.W.;

Ling M.H., Wang C.G., Wang D.C., Ch. C.W.;

Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).

-!- SIMILARITY BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.

EMBL; AF64821; AAD31592.1; --

EMSP; PO1494; 25.833.

InterPro: IPR003614; Knot1.

InterPro: IPR003614; Knot1.

InterPro; IPR003614; Knot1.

InterPro: PP000908; Scorpion_toxinL.

ProDom; PD000908; Scorpion_toxinL.

ProDom; Continuation of the continuation of the
                                                                                                                                                                                                                                                                                                                                                                                             76 GGTTACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEUROTOXIN AEP.
CCE46711BAF21DAC CRC64;
                                                                                                                      525028
                                                                                                                                                            Conservative:
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Matches:
Conservative:
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Indels:
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                                                                                                                                                                                                                                                                    JS-09-673-274B-2_COPY_1_132 (1-132) x Q95WX6 (1-85)
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Matches:
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             POTENTIAL.
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        1 21
22 82
85 AA; 9330 MW;
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85 AA; 9312 MW;
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55.26%
36.84%
30.52%
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81.50
55.26%
39.47%
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                                                                                                                                                Percent Similarity:
3est Local Similarity:
?uery Match:
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SIGNAL
CHAIN
SEQUENCE
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                                                                                                                   Pred. No.:
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STTT KONDON NA TANAN NA TANAN

RESULT 5

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MEDLINE=99397451; PubMed=10470850;
Raneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Kotani H.,
Raneko T., Katoh T., Sato S.,
Miyajima N., Tabata S.;
"Structural analysis of Arabidopsis thaliana chromosome 5. IX.
Sequence features of the regions of 1,011,550 bp covered by seventeen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 TCCTGCGTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGTGAGTGCAAGAGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 SerCysLeuTrpGly------AsnGluGlyCysAsnLysGluCysGlyAlaTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 23, Last annotation update)
01-MRR-2003 (TrEMBLrel. 23, Last annotation update)
Depressant insect toxin BmX [Tal precursor.
Mesobuthus marterial (Manchurian scorpion) (Buthus martensil).
Eukaryota: Metazoa; Atthropoda: Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Mesobuthus.
NCBI_TaxID=34649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=11437247, miege C., Dumas C., Cock J.M.; Two large Arabidopsis thallana gene families are homologous to the Brassica gene superfamily that encodes pollen coat proteins and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76 GGTTACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGCGAG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GlyAlaSerTyrGlyTyrCysTrpThrTrp---GlyLeuAlaCysTrpCysGlu 66
                                                                                                                                                                                                                                                                                                  POTENTIAL.
6CP567086032001A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-00T-2002 (TrEMBLrel. 22, Created) 01-0CT-2002 (TrEMBLrel. 22, Last sequence update) 01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
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SEQUENCE
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ID C8
SORRER REPRESENTATION OF STREET AND SERVICE AND SERVIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayme J.D., Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayme J.D., Adams M.D., Celniker S.E., Li P.W., Hoskinss R.A., Galle R.F., Adams H.D., Celniker S.E., Li P.W., Hoskinss R.A., Galle R.E., Adamstidas P.G., Scherer S.E., Li P.W., Hoskinss R.A., Garler S.D., R.A. Barder B.C., Rogers Y.-H.C., Blazelj R.G., Champe M., Pferifer B.D., R.A. Bardor R.C., Rogers Y.-H.C., Blazelj R.G., Chen J.X., Mixles G.L.G., Rand M.R., Boyle C., Barter E.G., Helt G., Nelson C.R., Mixles G.L.G., Rallew R.M., Basul A., Baswan B.P., Bardari D., Borter B.C., Buldwin D., R.A. Benos P.V., Berman B.P., Bardari D., Bolshakov S., Berkova D., Borchan M.R., Bouck J., Brytans B.P., Braddari D., Solshakov S., Borkova D., Borchan M.R., Bouck J., Brokstein P., Brottier P., Solshakov S., Berkova D., Borchan M.R., Bouck J., Brokstein P., Brottier P., Solshakov S., Banhke C., Cawley S., Danhke C., Cawenport L.B., Davies P., Cawley S., Danhke C., Cawenport L.B., Davies P., Broksor M., Cawley S., Danhke C., Cawenport L.B., Davies P., Bordsor R., Obup L.E., Downes M., Dagan Rockets S., Duxkov B.C., Dunn P., R.A. Bordsor R., Obup L.E., Downes M., Dagan Rockets S., Duxkov B.C., Dunn P., R.A. Houston K.J., Harvey D., Heiman T.J., Wein M.H., Ibegwam C., Retchum K.A., Howland T.J., Wein M.H., Ibegwam C., Rallen M.H., Ralush F., Kadira C., Katle C., Morleod J.R., Martei B., McIntesh T.G., Morley G., Morley G., Morley G., Morley B., Monnt S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., R.A. Reinson K.A., Romangton K., Saunders R.D.C., Scheeler F., Shen H.
                                                                                                                                                                                                                                                                                                                                                                                                                               16 TCCTGCGTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGTGACTGCAAGAGGAGG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                             C332274 protein.
C332274 protein.
C32226 OR CG10815 CR CG11520.
Drosophila metazoa Arthropoda, Hexapoda, Insecta, Pterygota,
Brasyota, Metazoa Arthropoda, Hexapoda, Hexapoda, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Epityfroidea, Brosophilidae, Drosophila.
                                                                                         POTENTIAL.
HYPOTHETICAL PROTEIN LCR46.
108DEAAE80969F55 CRC64;
  male component of the self-incompatibility response.";
                                                                                                                                                                                                                0 0 3 4 4 4 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0:-MAY-2000 (TrEMBLrel. 13, Created)
0:-CCT-2002 (TrEMBLrel. 22, Last sequence update)
6:-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                           Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 GSTTACAAGGGTGGTCACTGCGGTTCCTTCGCT 108
                                                                                                                                                                                                                                                                                                                                                                                  US-09-673-2748-2_COPY_1_132 (1-132) x P82761 (1-91)
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                                                                                                                                                                                                                Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                   Gaps:
                      Flant Mol. Biel. 46:17-34(2001).
EMBL; AB317061; -; NOT ANNOTATED CDS.
Hypothetical protein; Signa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                           9503 MM;
                                                                                                                                                                                                                               50.00
58.06
45.16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                               28
91 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-Berkeley;
                                                                                                                                                                                          Ailgnment Scores:
                                                                                                                                        SECUENCE
                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                               Ouery Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40ZA60
                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDZA60
                                                                                                                                                                                                                Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NA WATER
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34 GlySerCys-----AlaValTrpHisArgLysLysCysValAspIleCysGlnArg 50
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                                                                                                                                                                                                                                                                                                                                                                Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
Celniker S.E., Adams M.D., Ammaratides P.G., Brandon R.C., Rogers Y.,
A. Evans C.A., Gocayne J.D., Ammaratides P.G., Brandon R.Y., Busam D.A.,
Carlson J.M., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
Ibegwam C., Jahali M., Kruse D., Li P., Mattei B., Moshrefi A.,
McIncosh T.C., Moy M., Mirphy B., Nelson C., Nelson K.A., Nunco J.,
Racleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
Stapheron M., Strong R., Svirskas R., Tector C., Tyler D.,
Milliams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
Supmitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Hang Z.-Y., Wassarman D.A., Weinstock G.M., Weisenbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng I.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
Gibbs R.A., Wyers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GluGlyArgThrSerGlyHisCysSer----ProSerLeuLysCysTrpCysGlu 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misra S., Crosby M.A., Matthews E.B., Bayraktaroglu L., Campbell K. Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.J., Bergman C., Berman B., Carlson J.W., Celniker S.E., Clarp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Kronmiller B., Marshall B., Millburn G., Richter J., Russo S., Searle S.M.J., Smith E., Shu S., Smutnak F., Whitfield E., Ashburner M., Gelbart M.Y., Rubin G.M., Mungall C.J., Lewis S.E., "Annotation of Drosophila melanogaster genome."; Submitted (MAR 2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 AGGGGTTACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adams M.D., Ceiniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to the EMBL/GenBank/DDBJ databases.
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69 AA; 7720 MW; 87CC05D254A11AC4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69
4 4 4 5 2
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TyBase, FBgn0552268; CG32268.
InterPro; IPR0C2118; Gamma·thionin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (SEP-2002) to the EMBL, AE003477, AAF47764.2, HSSP, P41964, 1MYN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.50
51.28%
41.03%
29.40%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N. A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
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%FFFF80000×844FFF500444888

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Alignment Scores:
Pred. No.:
                                                                                                        Query Match:
                                                                                                                                                                                                                                                                                                                                                 09VZR2
                                                                                                                                                                                                                                                                                                                   RESULT :1
                                                                                                                                                                                                                                                                                                                                  Q9VZR2
                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                  TCCTGCGTGTGCGGTGCTGTGAACTACACTTCCGATTGCAACGGTGAGTGCAAGAGGAGG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 SerCysLeuPheGly-----AsnGluGlyCysAsnLysGluCysLysErTyr 49
QBWVS7;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Depressant insect toxin 2.
Leiurus quinquestriatus quinquestriatus (Egyptian scorpion).
Eukaryota; Metazoa; Archropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Leiurus.
                                                                                                                                                                              ZAKI T.1., Maruniak J.E.;

"Three polymorphic genee encoding LqqIT2 from the Egyptian scorpion Leiurus quinquestriatus.";

Leiurus quinquestriatus.";

Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).

SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).

InterPro: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.

InterPro: IPR002561, AAM74028.1;

InterPro: IPR002561, Scorpion_toxinL.

Pfam, PF00537; Loxin_3; 1.

SMART: SM00505; Knot1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 GGTTACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGCGAG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Megobuthus martensii (Manchurian scorpion) (Buthus martensii).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Megobuthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50 GlyGlySerTyrGlyTyrCysTrpThrTrp---GlyLeuAlaCysTrpCysGlu 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ling M., Wang C., Wang D., Chi C.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
--- SUBCELGULAR LOCATION: SECRETED (BY SIMILARITY)
--- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.
EMBL; AF073899; AAD41648.2;
HSSP; P01491; 183C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEPRESSANT INSECT NEUROTOXIN.
18E02CD791F3B5EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                               9099 MW; F13D53B18CDECBF0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   887
127
227
227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1999 (TrEMBLrel. 12, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JS-09-673-274B-2_COPY_1_132 (1-132) x Q8MVS7 (1-82)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Depressant insect neurotoxin precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003614; Knotl.
InterPro; IPR002061; Scorpion_toxinL.
Pfam. PF0057; toxin_3; 1.
SMART; SM00508; Scorpion_toxini; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85 AA; 9480 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                            0.127
76.50
55.26
39.47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                              82 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=34649;
                                                                                                                                 NCBI_TaxID=6885;
                                                                                                                                                                                                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91
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                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match:
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REATIN
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                                                                                                                                                                                                                                                                                                                                                                                                           --- AsnAspPheCysAspLysValCysLysSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 GlyGlySerTyrGlyTyrCysTrpThrTrp---GlyLeuAlaCysTrpCysGlu 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota: Metazoa, Arthropoda; Hexapoda: Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
   24 7 7 5 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel, 13, Created)
01-MAY-2000 (TrEMBLrel, 13, Last sequence update)
01-MAR-2003 (TrEMBLrel, 23, Last annotation update)
                                                                         Conservative:
Mismatches:
                                                                                                                                                                                                                                                             US-09-673-274B-2_COPY_1_132 (1-132) x 09Y1U3 (1-85)
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                                  Matches:
ength:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CG10812 protein (GH09576p).
CG10812.
                          76.50
55.268
36.848
28.658
                                                                                                                                                                                                                                                                                                                                                                                                               34 SerCysLeuTrpGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                         Percent Similarity:
Best Local Similarity:
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Length:

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Query Match:
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Q9VZR3
Pred. No.:
                                                                                                                                                                                                                              RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 AGGAGGGGTTACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGCGAG 129
                                                                                                                                                                                                                                                                                                                                                                                                        13 GGTTCCTGC---GTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGTGAGTGCAAG 69
                                                                                                                                                                                                                                                                                                                                                                                                                           GluGluGlyArgSerSerGlyHisCysSer---- ProSerLeusysCysTrpCysGlu 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

COTORA M., COTORAS F., Merino E., Becerril B., Antunez S.R.,
COTORA M., COTORAS F., Merino E., Becerril B., Antunez S.R.,
A GATTA D.E., Possani L.D.
T. Grana D.E., Possani L.D.
T. Darticularly affects Na+-channels of rat peripheral ganglia preparations.";
Darticularly affects Na+-channels of rat peripheral ganglia preparations.";
C. SUBCELULAR LOCATION: SECRETED (BY SIMILARITY)
C. SUBCELULAR LOCATION: SECRETED (BY SIMILARITY)
C. SUBCELULARITY: BALGOOR TO THE ALPHA/BETA-SCORPION TOXIN PAMILY.
REMBL, AFBB171; AALS72911.;
RICHEPPO; IPR003614; Knot1:
RICHEPPO; PR003614; SCORPION LOXÍNE.
                                                              Stableton M., Brokstein P., Hong L., Agbayani A., Carlson J., Charpe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Krommlier B., Li P., Liao G., Miranda A., Mingail C.J., Nunoo J., Pacleb J., Paragus V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Centruloides limpidus limpidus (Mexican scorpion).
Eukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Scorpiones,
Buthoidea, Buthidae, Centruroides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
NA+-CHANNEL MODIFYING TOXIN.
21018F12E2ECC26E CRC64;
                                                                                                                                             Submirred (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AE03477; AAK47757.1; -.
EMBL, AAV180762; AAK50622.1; -.
ENSEP; P41364; AMS0622.1; -.
FlyBase; FBgn0035434; CG10812.
InterFro; IPR002118; Gamma-thionin.
Prodon: P0302534; Gamma-thionin. 1:
SEQUENCE 69 AA, 7656 MW, 72555FDBB1DCC6F7 CRC64;
                                                                                                                                                                                                                                                                                    69
15
16
3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01 MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Na+-crannel modifying toxin precursor.
of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                US 09 673-2748-2_CCPY_1_132 (1-132) x Q9VZR2 (1-69)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probom, PD00537; toxin 3; 1.
Probom, PD000908; Scorpion toxinL; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19
82
9198 MW;
 "The genome sequence of Dro
Science 287:2185-2195(2000)
                                                                                                                                                                                                                                                                                   0.236
74.50
42.508
37.508
27.908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00505; Knotl; 1.
Signal.
SIGNAL. 1 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 AA;
                                      FRCM N.A.
                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI TaxID=29941;
                                                         STRAIN-Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
                                                                                                                                                                                                                                                                      Alignment Scores:
Pred. No.:
Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                         SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CBWRY4;
                                                                                                                                                                                                                                                                                                                                           Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRWRY4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLL9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8WRY4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S
```

Alignment Scores:

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TISSUE-Venom gland;

AT IN W.-X., Zeng X.-C., Zu S.-Y.;

Li W.-X., Zeng X.-C., Zu S.-Y.;

Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.

CC -1 SINGLELULUAR ALOKATION: SECRETED (BY SIMILARITY).

C1 SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.

EMBL; AF150C09; AAG09657.1; -..

RINGLEPO, IPRO01219; Neurolo.

RRINTS: PRO01284; TOXIN.

RRINTS: RRO01284; TOXIN.

RODON; PRO00508; Sccrpion_toxinL; 1.

SMART; SMO0505; MAOLI.

SMART; SMO0505; MAOLI.

SMART; SMO0505; MAOLI.

SMART; SMOOFS; MAOLI.

SEQUENCE 85 AA; 9426 MW, 6EFC463E02E95091 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 TGCAACGGTGAGT&CAA&AGGAGGGGTTACAAGGGTGGTCACTGC------GGTTCC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19 TGCGTGTGGGGTGCTGTGAACTACACTTCCGAT-----TGCAACGGTGAGGGAGGG 72
                                                                                                                                                                                                                                        31 CysThrLeuAlaCysIleAspLysThrGlyAspLysAsnCysAspArgAsnCysLysLys 50
                                                                                                                                                                                                                                                                                             73 AGGGGTTACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGCGAG 129
                                                                                                                                                                                                                                                                                                                                     51 GluG.yGlySerPheGlyHisCysSerTyrSerAla-----CysTrpCysLys 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                OGGUA7;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 9.4 kDa protein.
Mesobuthus martensii (Manchurian scorpion) (Buthus martensii).
Bukaryota: Metazca; Arthropoda; Chelicerata; Arachnida; Scorpiones;
Buthoidea; Buthidae; Mesobuthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein.
5 AA; 9426 MW; 6EFC463E02E95091 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246612
  Q9V2R3;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
                       Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-673-274B-2_CCPY_1_132 (1-132) x Q9GUA7 (1-85)
                                                                                                                                                          US-09-673-274B-2_COPY_1_132 (1-132) x Q8WRY4 (1-84)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                  85 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indel8:
                                                                                          Indels:
                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103 TTCGCTAACGTGAACTGCTGGTGC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ::: |||:
TyrGlyAsnAla---CysTrpCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.278
74.00
64.29$
42.86$
27.72$
0.238
74.50
48.72%
35.90%
27.90%
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                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                          Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1245E
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85 A.

PRT;

PRELIMINARY;

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SEQUENCE FROM N.A.
STRAIN=10: ITSSE=Veron gland;
MEDLINE=20:91122; Pubwed-10728828;
Zeng X.C., Li W.X., Zhu S.Y., Peng F., Jiang D.H., Yang F.H., Wu K.E., Zeng X.C., Li W.X., Zhu S.Y., Peng F., Jiang D.H., Yang F.H., Wu K.E., Zeng X.C., Li W.X., Zhu S.Y., Peng F., Jiang D.H., Yang F.H., Wu K.E., Zeng X.C., Li W.X., Zhu S.Y., Peng F., Jiang D.H., Yang F.H., Wu K.E., Zeng X.C., Li W.X., Zhu S.Y., Peng F., Jiang D.H., Yang F.H., Wu K.E., Town Chinese scorpton Buthus martensii Karsch (BmK).";
Toxicon 38:893-899(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mesobuthus martensii (Vanchurian scorpion) (Buthus martensii).
Eukaryota, Metazoa, Arthropoda, Chelicerata, Arachnida, Scorpiones,
Buthoidea, Buthidae, Mesobuthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
101-DAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative sodium channel toxin BMKT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD000908; Scorpion_toxinU; 1.
SMART; SM00505; Knot1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=34649;
                                                                                                                                                                                                                                                                                                    095P69
                                                                                                                                                                                                                                      RESULT 15
1095P69
AC 095P69
DT 01-DE DT
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                                                                                                                       ठ
                                                                                                                                                                                                                                                                                                             MEDLINE-20196006; PubMed=10731132;
Addams M.D. Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D., Addams M.D., Celniker S.E., Holf R.A., Hoskins'R.A., Galle R.F., Garler R.S., Scherer S.E., Ii P.H., Hoskins'R.A., Galle R.F., Garler B.D., Wortman J.R., Yandrads S., Ashburner M., Henderson S.N., Sutron G.G., Wortman J.R., Yandrads R.G., Champe M., Pfeiffer B.D., Warman J.R., Yandrads R.G., Champe M., Pfeiffer B.D., Warman J.R., Barade R.G., Champe M., Pfeiffer B.D., Warman J.R., Barade B.G., Nelson C.R., Mikios G.L.S., Abril J.F., Agbayari A., Barandale J., Bardari D., Beasiey E.M., Benos P.V., Berman B.P., Bardari D., Bockhakov S., Benkova D., Boccham M.R., Bouck J., Brokstein P., Brottler P., Brottler P., Bortler P., Brottler P., Brottler P., Bouch S., Dallackov S., Dunkov B.C., Dunn P., Burbin R.J., Evangelista C.C., Ferraz C., Center A., Chandra I., Bouch S., Doup L.E., Downes M., Dugan Rocha S., Purkov B.C., Dunn P., Bouchin R.J., Evangelista C.C., Ferraz C., Gelbart M.M., Glasser K., Gabriellan A.B., Gary N.S., Gabart M.M., Glasser K., A. Houston K.A., Howland T.J., Wer M.-, Houck J., Houston K.A., Howland T.J., Wer M.-, Houck J., Houston K.A., Howland T.J., Wer M.-, Houck J., Lais Y., Lin X., Martei B.E., Kodira C.D., Kraft C., Morris J., Wosherson D., Lai Y., Levitsky A.A., Li J. J., J. Z., Liang Y., Lin X., Lasko P., Lei Y., Levitsky A.A., Li J., J., J., J., Men H., Pollard J., Martei B., McIntosh T.C., McLeod M.P., Puri V. Wartei B., Martei B., McIntosh T.C., McLeod M.P., Puri V. Wartei B., Martei B., McIntosh T.C., McLeod W.P., Puri V. Wartei B., Martei B., Martei B., McIntosh T.C., McLeod W.P., Puri V. Wartei B., Martei B., Spradling A.C., Stapleton M., Stung R., Sun E., Spradling A.C., Zhon M., Wartei B., Martei B., Zhori J., Zhon W., W
                                                                                                        Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endoptery, Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                106 AA; 11598 MW; A76479D6E44BC50C CRC64;
01-MAR-2003 (TrEMBLrel. 23, Last annotation update) G010813 procesin.
CG32279 OR CG10813.
Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002118; Gamma-thionin.
InterPro; IPR003614; Knot1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD002594; Gamma-thionin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE003477; AAF47756.1; -
HSSP; P41964; 1MYN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FlyBase: FBgn0052279; CG32279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Knot 1;
                                                                                                                                                                                                                                      [1] SEQUENCE FROM N.A. STRAIN=BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SM00505;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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4 AAGCTTATCGGTTCCTGC---GTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGT 60
 106
16
3
17
7
 Length:
Matches:
Conservative:
                                                                                  US-09-673-274B-2_COPY_1_132 (1-132) x Q9VZR3 (1-106)
                                     Mismatches:
                                                 Indels:
0.328
73.50
44.198
37.218
                                              27.53
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Best Local Similarity:

Query Match:

Percent Similarity:

Pred. No.:

68 LysTyrLysGlyProCysAlaValTrpAsp-----AsnGluMetCysArgArg 83

9 ਨੇ

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52 TGCAACGGTGAGTGCAAGAGGAGGGTTACAAGGGTGGTCACTGC------3GTTCC :02
                                                                                                                                                                                                         9412 MW; 2FFC463EC2EE57E1 CRC64;
                                                      12
12
7
                                                                                    Conservative:
                                                                                                                                                            US-09-673-274B-2_COPY_1_132 (1-132) x Q95P69 (1-85)
                                                                                                  Mismatches:
                                                      Length:
Matches:
                                                                                                                  indels:
                                                                                                                                                                                                                                                                                                                           Search completed: October 16, 2003, 17:16:13 Job time : 40.0299 secs
                                                                                                                                                                                                                                                  103 TTCGCTAACGTGAACTGCTGGTGC 126
                                                                                                                                                                                                                                                                                61 TyrGlyAsnAla --- CysTrpCys 67
                                                     0.518
72.00
60.71%
42.86%
26.97%
            85 AA;
                                                                                                  Best Local Similarity:
                                                                                    Percent Similarity:
channe]
                                       Alignment Scores:
            SEQUENCE
                                                                                                                  Query Match:
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nucleic

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equence:

searched:

Sequence 2, Appl. Sequence 4, Appl. Sequence 2, Appl. Sequence 6, Appl. Sequence 6, Appl. Sequence 8, Appl. Sequence 8, Appl.

Sequence 13, Appl Sequence 11, Appl Sequence 9, Appli

App Appi Appi Appi Appi Appi Appi

Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence

Sequence 410,

Seguence

Sequence 8, Sequence 41

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Sequence 119
Sequence 119
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Sequence 119
September 119
Septembe
                                                                           155.09 429.481.2

155.09 429.481.2

155.00 180.247.4

155.10.180.247.4

155.10.180.247.6

155.10.178.213.411

155.10.178.213.411

155.10.178.213.411

155.10.178.213.440

155.10.178.213.440

155.10.264.480.10

155.10.178.213.460

155.10.178.213.460

155.10.178.213.460

155.10.178.213.460

155.10.178.213.160

155.10.178.213.160

155.10.178.213.160

155.10.178.213.160

155.10.178.213.160

155.10.178.213.308

155.10.178.213.308

155.10.178.213.308

155.10.178.213.308

155.10.178.213.308

155.10.178.213.308

155.10.178.213.308

155.10.178.213.308

155.10.178.213.308

155.10.178.213.308

155.10.178.213.308

155.10.178.213.308

155.10.178.213.308

155.10.178.213.318

155.10.178.213.318
US-10-125-258-119
US-10-125-258-117
US-10-264-480-11
US-10-264-480-11
US-10-264-480-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL : GNMENTS
   999964499988999
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LENGTH: 44
TYPE: PRT
   232
232
79.5
79.5
76.5
                                                                                      74.5
74.5
74.5
74.5
71.5
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                                                                                                                                                                                                                                                                                                                                                                          68.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 1
     O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               October 16, 2003, 17:12:07 ; Search time 27.4086 Seconds (without alignments) 1578.850 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                            gataagcttatcggttcctg......tgaactgctggtgcgagact 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published Applications AA:•

1: /cgn2_6/ptodata/2/pubpaa/US37_PUBCOMB.pep:•
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW PUB_pep:•
3: /cgn2_6/ptodata/2/pubpaa/US36_PUBCOMB.pep:•
4: /cgn2_6/ptodata/2/pubpaa/US36_PUBCOMB.pep:•
5: /cgn2_6/ptodata/2/pubpaa/US36_PUBCOMB.pep:•
6: /cgn2_6/ptodata/2/pubpaa/US36_PUBCOMB.pep:•
7: /cgn2_6/ptodata/2/pubpaa/US36_PUBCOMB.pep:•
8: /cgn2_6/ptodata/2/pubpaa/US36_PUBCOMB.pep:•
9: /cgn2_6/ptodata/2/pubpaa/US36_PUBCOMB.pep:•
10: /cgn2_6/ptodata/2/pubpaa/US36_PUBCOMB.pep:•
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13: /cgn2_6/ptodata/2/pubpaa/US36_PUBCOMB.pep:•
13: /cgn2_6/ptodata/2/pubpaa/US309_PUBCOMB.pep:•
14: /cgn2_6/ptodata/2/pubpaa/US306_PUBCOMB.pep:•
15: /cgn2_6/ptodata/2/pubpaa/US306_PUBCOMB.pep:•
16: /cgn2_6/ptodata/2/pubpaa/US306_PUBCOMB.pep:•
16: /cgn2_6/ptodata/2/pubpaa/US306_PUBCOMB.pep:•
17: /cgn2_6/ptodata/2/pubpaa/US306_PUBCOMB.pep:•
18: /cgn2_6/ptodata/2/pubpaa/US306_PUBCOMB.pep:•
17: /cgn2_6/ptodata/2/pubpaa/US306_PUBCOMB.pep:•
18: /cgn2_6/ptodata/2/pubpaa/US306_PUBCOMB.pep:•
               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                     hits matisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                       609560 segs, 163917102 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                            US-09-673-274B-2_COPY_1_132
267
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                          0.0
0.7
0.5
0.5
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Sequence 441, App Sequence 7787, App Sequence 395, App Sequence 12, App Sequence 167, App Sequence 167, App Sequence 22, Appl Sequence 22, Appl Sequence 23, Appl Sequence 39, Appl

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79.50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GATAAGCTTATCGGTTCCTGCGTGTGGGGGTGCTGTGAACTACTCGGATTGCAACGGT 60
                                                                                                                                                                                                                                                                                                                                                                                                SpyalHislleGlySerCysValTrpGlyAlaValAspTyTTnrSerAsnCysAsnAsn 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
3 10 125-258-117
5 Sequence 117, Application US/10125258
6 Publication No. US2030028920A1
6 RENEAL INPORMATION:
APPLICANT Attier, Daniel J.
APPLICANT Herrmann, Rafael
APPLICANT: Meaver, Januel L.
APPLICANT: Weaver, Januel L.
APPLICANT: Wea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-673 274B 2_COPY_1_132 (1-132) x US-10-125-258-117 (1-73)
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Matches:
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Matches:
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Mismatches:
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US:10-125-258-117
CRGANISM: Agrotis ipsilon
US-10-125-258-119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 TGGTGCGAG 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
Query Match:
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; ORGANISM: Scolopendra canidens DS-US-09-829-481-2
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                        APPLICANT: INCOGRAPIONE
APPLICANT: Inceedlu, Bora
APPLICANT: Inceedlu, Bora
TITLE OF INVENTION: ISCLATED POLYPEPTIDES AND COMPOSITIONS
TITLE OF INVENTION: FROM THE VENOM OF P. TRANSVAALICUS AND METHODS OF USE
FILE REFERENCE: UCAL256
CURRENT APPLICATION NUMBER: US/10/264,48C
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: 60/393,070
PRIOR FILING DATE: 2002-06-28
PRIOR FILING DATE: 2001-10-04
PRIOR FILING DATE: 2001-10-04
SRIOR FILING DATE: 2001-10-04
SRIOR FILING DATE: 2001-10-04
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 CysPheTrpLeuGlyLysAsn-----GluAsnCysAspLysGluCysLysAslaLysAsn 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 TCCTGCGTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGTGAGGTGCAAGAGGAGG 75
                                                                              19 TGCGTGTGGGGGTGCTGTGAACTACACTTCCGATTGCAACGGTGAGTGCAAGAGAGGGGGT 78
                                                                                                                                                          79 TACAAGGGT-----GGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGCGAG 129
                                                                                                                                                                                            34 GlnGlyGlySerTyrGlyTyrCysTyrSerPheAla-----CysTrpCysGlu 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 GGTTACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGCGAG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 GlyGlySerTyrGlyTyrCysTrpThrTrp---GlyLeuAlaCysTrpCysGlu 45
                                        IS-09-673-274B-2_COPY_1_132 (1-132) x US-10-264-480-11 (1-66)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JS-09-673-274B-2_COPY_1_132 (1-132) x US-10-264-480-9 (1-61)
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Matches:
Conservative:
Mismatches:
Indels:
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ORGANISM: Leiurus quinquestriatus quinquestriatus
IS-10-264-480-9
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15-09-829-481-2

Sequence 2, Application US/09829481

Sequence 2, Application US/09829481

Setent No. US20020069427A1

GENERAL INFORMATION:
APPLICANT: Weng, Zude
APPLICANT: Weng, Zude
APPLICANT: Weng, Zude
APPLICANT: Weng, James
TITLE OF INVENTION: Arthropod Defensins
FILE REFERENCE: BB1441 US NA
FURRENT FILING DATE: 2001-04-10

PRIOR FILING DATE: 2000-04-10

PRIOR FILING DATE: 2000-04-14

NUMBER OF SEQ ID NOS: 11
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    Gaps:
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SEQ 1D NO 2
LENGTH: 61
TYPE: PRT
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APPLICANT: DeBose, Richard
APPLICANT: Perseinnet, Georges
APPLICANT: Hoffman, Jules
TITLE OF INVENTION: Chimeric Gene Encoding Drosomycin,
TITLE OF INVENTION: Chimeric Gene Encoding Drosomycin,
TITLE OF INVENTION: Transgenic Plants
FILLE REFERENCE: A32899-PCT-USA-A-A 072667.0182
CURRENT FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: US/16/180,247
CURRENT FILING DATE: 1998-07-08
PRIOR FILING DATE: 1998-07-08
PRIOR FILING DATE: 1998-07-08
PRIOR FILING DATE: 1998-07-08
PRIOR FILING DATE: 1997-07-11
PRIOR FILING DATE: 1997-07-11
PRIOR FILING DATE: 1997-07-11
PRIOR FILING DATE: 1997-07-11
PRIOR FILING DATE: 1997-07-14
PRIOR FILING DATE: 1997-07-24
PRIOR FILING DATE: 1997-07-14
PRIOR FILING DATE: 1997-07-14
PRIOR FILING DATE: 1997-07-14
                                                                                                                                                                                                                                                                                                                            49 GATTGCAACGGTGAGTGCAAGAGGAGGGGTTACAAGGGTGGTCACTGCGGTTCCTTCGCT : 08
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                                                                                                                                                                                                                                                                                                                                                                     34 GluCysAsnArgHisCysArgGlyAsnSlyPheThrGlyGlyTyrCysThrGlyPheLeu 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13 GGTTCCTGC---GTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGTGAGGTGCAAG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 GlyProCysAlaValTrpAsp-----AsnGluThrCysArgArgValCysLys 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 GluGluG.yArgSerSerGlyH.sCysSer----ProSerLeuLysCysTrpCysGlu 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-673-274B-2_COPY_1_132 (1-132) x US-10-180-247-4 (1-44)
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Length:
Matches:
Conservative:
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Gaps:
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; Sequence 7, Application US/10264480; Publication No. US20030113892A1; GENERAL INFORMATION:
, ORGANISM: Drosophila melanogaster
US-10-180-247-2
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US-10-264-480-7
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US-10-180-247-2

US-10-180-247-2

Sequence 2, Application US/1018c247

Sequence 2, Application US/2018c247

Publication No. US2003167519A1

GENERAL INFORMATION:
APPLICANT: DeRose, Richard
APPLICANT: Hoffman, Jules

TITLE OF INVENTION: Chimeric Gene Encoding Droscmycin,
TITLE OF INVENTION: Chimeric Gene Encoding Droscmycin,
TITLE OF INVENTION: Chimeric Gene Encoding Droscmycin,
TITLE OF INVENTION: Vector Containing it and Production of Disease-Resistant
TITLE OF INVENTION: Transgenic Plants
FILLE REFERENCE: A32889-PCT-USA-A-A 072667.0182

CURRENT FLING DATE: 2002-06-26

PRIOR FLING DATE: 2002-01-11

PRIOR FLING DATE: 1998-00-11

PRIOR FLING DATE: 1998-00-11

PRIOR FLING DATE: 1999-07-24

NUMBER CF SEQ ID NOS: 15

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 70
             GENERAL: Freysinnet, Georges
APPLICANT: Preysinnet, Georges
APPLICANT: Freysinnet, Georges
APPLICANT: Freysinnet, Georges
APPLICANT: Hoffman, Jules
ANDERSION: Transgenic Plants
FILE REFERENCE: A12889-PCT-USA-A-A 072667.0152
CURRENT APPLICATION NUMBER: C9/480,251
PRIOR APPLICATION NUMBER: C9/480,251
PRIOR APPLICATION NUMBER: PCT/FR99/01462
PRIOR APPLICATION NUMBER: FR97/09,115
PRIOR APPLICATION NUMBER: FR97/09,115
PRIOR FILING DATE: 1997-07-11
PRIOR FILING DATE: 1997-07-11
PRIOR APPLICATION NUMBER: FR97/09,663
PRIOR FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 AGGAGGGTTACAAGGGTGGTCACTGCGGTTCUTTCGCTAACGTGAACTGCTGGTGCGAG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13 GGTTCCTGC---GTGTGGGGTGCTGTSAACTACACTTCCGATTGCAACGGTGAGTGCAAG 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTHER INFORMATION: Ubiquitin drosomycin fusion peptide IS 10 190 247 6
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Matches:
Conservative:
Mismatches:
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Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.387
74.50
42.50%
37.50%
27.90%
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                              SEÇ ID NO 6
LENGTH: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.:
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US-10-264-480-6

| Sequence 6, Application US/10264480
| Sequence 6, Application US/10264480
| Publication No. US2C30113892A1
| Publication No. US2C30113892A1
| Publication No. US2C30113892A1
| APPLICANT: Hammock, Bruce D. APPLICANT: Hammock, Bruce D. TITLE OF INVENTION: ISOLATED POLYPEPTIDES AND COMPOSITIONS
| TITLE OF INVENTION: FROM THE VENOM OF P. TRANSVAALICUS AND METHODS OF USE | TITLE OF INVENTION: FROM THE VENOM OF P. TRANSVAALICUS AND METHODS OF USE | CURRENT APPLICATION NUMBER: US/10/264,480 | CURRENT FILING DATE: 2002-10-04 | PRIOR PETLING DATE: 2002-06-28 | PRIOR PETLING DATE: 2002-06-28 | PRIOR FILING DATE: 2001-0-04 | NUMBER OF SEQ 1D NOS: 30 | SOFTWARE: FastSEQ for Windows Version 4.0 | SOFTWARE: FastS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 AGGAGGGGTTACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGCGAG 129
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APPLICANT: Hammock, Bruce D.
TITLE OF INVENTION: ISOLATED POLYPEPTIDES AND COMPOSITIONS
TITLE OF INVENTION: FROM THE VENOM OF P. TRANSVAALICUS AND METHODS OF USE
FILE REFERENCE: UCAL256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 TCCTGCGTGTGGGGGGGGGGAACTACAATTGCAACGGTGAACGGAAGAGGAGG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----AsnGluGlyCysAspLysGluCysLysAlaTyr 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 GGTTCCTGC---GTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGTGAGTGCAAG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----AsnGluThrCysArgArgValCysLys 50
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                                                                                                                                                                                                                                                                                                                                               US-09-673-2748-2_COPY_1_:32 (1-132) x US-10-180-247-2 (1-70)
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Mismatches:
Indels:
Length:
Matches:
Conservative:
Mismatches:
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Matches:
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RESULT 13
US-10-178-213-411
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Publication No. US20030113892A1
Sequence 8. Application US/10264485
Publication No. US20030113892A1
SERBRAT HARCRANTION:
APPLICANT: Hammock, Bruce D.
APPLICANT: Hommock, Bruce D.
APPLICANT: Inceeglu, Bora
TITLE OF INVENTION: ISOLATED POLYPEPTIDES AND COMPOSITIONS
TITLE OF INVENTION: ISOLATED POLYPEPTIDES AND METHODS OF USE
FILE REFERENCE: USAL256
CURRENT APPLICATION NUMBER: US/10/264,480
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: 60/327,602
PRIOR APPLICATION NUMBER: 60/327,602
PRIOR APPLICATION NUMBER: 60/327,602
PRIOR APPLICATION NUMBER: 60/327,602
PRIOR FILING DATE: 2001-10-04
SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
DENGTH: 61
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Matches:
Conservative:
Mismatches:
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Mismatches:
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Matches:
CURRENT APPLICATION NUMBER: US/10/264,480
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: 60/93,070
PRIOR FILING DATE: 2002-06-28
PRIOR FLING DATE: 2001-0-04
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
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55.26%
36.84%
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71.50
55.26$
36.84$
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ORGANISM: Buthus occitanus
S-10-264-480-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Buthus occitanus IS-10-264-480-8
                                                                                                                                                                                                                                                                                                                                          0.932
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Sest Local Similarity:
Query Match:
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est Local Similarity:
uery Match:
                                                                                                                                                                                                                                                                                                                   lignment Scores:
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13 GGTTCCTGCGTGTGGGGGTGCTGTGAACTACACTTCCGATTGCAACGGTGAGTGCAAGAGG 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 AGGGGTTACAAGGGTGGTGCTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 GluGlyPheTyrGlyGlyH:sCysArgGlyPheArgHis-- ArgCysPheCys 43
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APPLICANT: Simmens. Carl R.
APPLICANT: Navarro Acevedo, Pedro A.
APPLICANT: Navarro Acevedo, Pedro A.
APPLICANT: Cahoon, Rebecca
APPLICANT: Cahoon, Rebecca
APPLICANT: Lu, Albert
APPLICANT: Lu, Albert
APPLICANT: Wongo, James
ITLE OF INVENTION: Defensin Polynucleotides and Methods of
ITLE OF INVENTION: Defensin Polynucleotides of
FILE REFERENCE: 35118/246703
CURRENT FILING DATE: 2002-06-22
PRIOR APPLICATION NUMBER: 60/300,152
PRIOR APPLICATION NUMBER: 60/300,241
PRIOR FILING DATE: 2001-06-22
PRIOR FILING DATE: 2001-06-22
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                    APPLICANT: Navarro Acevedo, Pedro A. APPLICANT: Navarro Acevedo, Pedro A. APPLICANT: Harvell, Leslie APPLICANT: Cahoon, Rebecca APPLICANT: Cahoon, Rebecca APPLICANT: Cahoon, Reacca APPLICANT: Lu, Albert Billy Fred APPLICANT: Hu, Albert Band: Rafael, APPLICANT: Hong, James TITLE OF INVENTION: Defensin Polynuciectides and Methods of TITLE OF INVENTION: Use FILE REFERENCE: 3514244733 CURRENT APPLICATION NUMBER: 60,100,152 PRIOR APPLICATION NUMBER: 60,100,152 PRIOR FILING DATE: 2001-06-22 PRIOR FERSESO for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-673-2748-2_CCPY_1_132 (1-132) x US-10-178-213-411 (1-47)
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Mismatches:
Indels:
                                                                                         APPLICANT: Simmons, Carl R.
APPLICANT: Navarro Acevedo, Pedio A.
APPLICANT: Harvell, Leslie
APPLICANT: Cahoon, Rebecca
APPLICANT: McGutcher, Billy Fred
APPLICANT: Lu, Albert
APPLICANT: Herrmann, Rafae;
Sequence 411, Application US/13178213; Publication No. US2030041348A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 410, Application US/10178213; Publication No. US20030041348A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.05
71.00
50.00$
36.84$
26.59$
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ORGANISM: Tropaeolum majus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
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US-10-178-213-410
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Search completed: October 16, 2003, 17:34:08 Job time : 28.4086 secs

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13 GGTTCCTGCGTGTGGGGGGGTGCTGTGAACTTCCGATTGCAACGGTGAGTGCAAGAGG 72
                                                                                                                                                                                                                                                                                                             42 GlyProCysVal-----SeiLysThrAshCysAlaSerValCysLysThr 56
                                                                                                                                                                                                                                                                                                                                                   73 AGGGGTTACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGG 126
                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION US/10.78213

PUBLICATION NO. US2030041348A1

GENERAL INFORMATION:

APPLICANT: Simmens, Carl R.

APPLICANT: Harvell Leslie

APPLICANT: Gracon, Billy Fred

APPLICANT: Lu, Albert

APPLICANT: Lu, Albert

APPLICANT: Herrann, Rafael

APPLICANT: Herrann, Rafael

APPLICANT: Herrann, Rafael

APPLICANT: Herrann, Rafael

APPLICANT: Wordy. Johnson, 10.6

ITLE OF INVENTION: Defensin Polynuclectides and Methods of

ITLE OF INVENTION: Defensin Polynuclectides

CURRENT APPLICATION NUMBER: 80/300,178,213

CURRENT APPLICATION NUMBER: 60/300,241

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEC 12 NOS: 469

SOFTWARE: FASTSEQ for Windows Version 4.0

LEWITH APPLICATION NUMBER: 60/300,241
                                                                                                                                                                                                                                           US-09-673-274B-2_COPY_1_132 (1-132) x US-10-178-213-410 (1-77)
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20
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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71.00
50.00%
36.84%
26.59%
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70.50
59.26%
37.04%
26.40%
; SEG ID NO 410

: LENGTH: 77

: TYPE: PRT

: ORGANISM: Tropaeolum majus

US-10-178-213 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
CRGANISM: Glycine max
US-10-178-213 387
                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
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US-10-178-213_387
                                                                                                      Alignment Scores:
Pred. No.:
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Pred. No.:
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6, Appl 6, Appl 0063, A 9, Appl

Sequence Sequence Sequence

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Sequence 2

Sequence Seguence

Sequence 2

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APPLICANT: Hammock, Bruce D.
APPLICANT: Herrmann, Rafael
APPLICANT: Mcscowitz, Haim
TITLE OF INVENTION: Insect Control With Multiple Toxins
NUMBER OF SQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: 0.0...

ZIP: 94111-4121

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-305/MS-DOS
SOFTWARE: Patentin Pelease #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,046
FT::NG DATE: 08-MAY-1995
US 06-435 C4C-3
US-09-220-216-3
US-08-952-333A-14
US-08-970-264A-27
US-08-970-264A-27
US-08-970-264A-27
US-08-682-465A-26
US-09-252-991A-2063
US-09-465-309-19
US-08-465-309-19
US-08-465-49-2
US-08-465-49-2
US-09-252-991A-31433
US-09-252-991A-3162
US-09-252-991A-22787
US-09-053-021-4
US-09-053-031-2
US-09-252-991A-22787
US-09-252-991A-22334
US-08-312-384-20
US-08-312-384-20
US-08-312-384-20
US-08-312-384-20
US-08-312-384-20
US-08-312-384-20
US-08-312-384-20
US-08-312-384-20
US-08-312-384-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Majestic, Parsons, Siebert & Hsue STREET: Four Embarcadero Center, Suite 1450 CITY: San Franciso Courte: California COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Slebert, J. Suzanne
RZGISTRATICN NUMBER: 28,759
REFERENCE/DOCKET NUMBER: 2500.078USO
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1
US-08-435-040-2
Sequence 2, Application US/08435040
; Parent No. 5756340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (415) 362-5556
TELEFAX: (415) 362-5418
TELEX: 278638 MGPS
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Hammool
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
88
      'Ommand line parameters:

**MODEL-frame*-n2P model - DEV=x1p

**MODEL-frame*-n2P model - DEV=x1p

**DE-specific - DEV=x1p

**DES=x1p

**DES=x1p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Appli
Sequence 4, Appli
Sequence 25, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 25, Appl
Sequence 16810, A
Sequence 32270, A
Sequence 6, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Appli
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849.038 Millon cell updates/sec
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                                                                                                                                                     October 16, 2003, 17:06:37; Search time 13:1561 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lssued_Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/pcTuS_COMB.pep:*
                        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compuger Ltd.
                                                                                                      nucleic - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-435-040-2
US-09-020-216-2
US-08-882-485A-25
US-08-933-314-25
US-09-480-251-4
US-09-480-251-6
US-09-480-251-5
US-09-480-251-6
US-09-400-251-0
US-09-252-991A-16810
US-09-252-991A-32270
US-08-252-991A-32270
US-08-451-472-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 otal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                            US-09-673-274B-2_COPY_1_132
267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0#
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                       0.5
                                                                                                                                                                                                                                                                                                                                                Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               finimum DB seq length: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query
Match Length
                                                                                                                                                                                                                                                                                                                              BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            erfect score:
                                                                                                                                                                                                                                                                                                                              coring table:
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                                                                                                                                                                                                                                            itle:
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65 7 9 9

Conservative: Mismatches: Indels:

Gaps:

Length: Matches:

N

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70 AGGAGGGTTACAAGGGTGGTCACTGC-----GGTTCCTTCGCTAACGTGAACTGC 120
                                                                                                                                                                                                                                                                                                                                                                                29 LysAsnGlyAlaGluSerGlyTyrCysGlnTrpPheGlyLysTyrGlyAsnAla---Cys 47
                                                                                                                                                                                                                                                                                                                                                     16 TCCTGCGTGTGG-----GGTGCTGTGAACTACACTTCCGATTGCAACGGTGAGTGCAAG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-C8-682-485A-25
Sequence 25, Application US/06682485A
Patent No. 5763568
Patent No. 5763568
PAPLICANT: ATKINSON, RONALD K
APPLICANT: ATKINSON, RELIN E.H.
APPLICANT: TYLER, MARGARET I
APPLICANT: VONARX, EDWARD J
TITLE OF INVENTION: Insecticidal Toxins Derived From
TITLE OF INVENTION: Ennel Web (Atrax or Hadronyche Spiders)
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                       US-09-673-274B-2_CCPY_1_132 (1-132) x US-09-020-216-2 (1-65)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,485A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/682,485
FILING DATE: 17-UCLX-1996
APPLICATION NUMBER: AUS/08/256,933
FILING DATE: 27-ULX-1994
APPLICATION NUMBER: WO 93/15108
FILING DATE: 29-JAN-1993
APPLICATION NUMBER: AU PL0722
FILING DATE: 31-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2: Zeneca, Inc.
1200 South 47th Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PPD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-231-1542
TELEFAX: 510-231-1112
INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38,301
                                                                  N-terminal
                                                                                                                                                                          80.50
57.14%
40.48%
30.15%
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  peptide
NO
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: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 TGGTGC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||||.|
48 TrpCys 49
                                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Richmond
STATE: Californ
MOLECULE TYPE: )
HYPOTHETICAL: NO
HYPOTHETICAL: NO
HYPOTHETICAL: NO
FRAGMENT TYPE: 1
US-09-020-216-2
                                           8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 AsnCysValTyrThrCysGlyAlaAsnSerTyr ...----CysAsnThrGluCysThr 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 LysAsndlyAlaGluSerGLyTyrCysGlnTrpPheGlyLysTyrGlyAshAla---Cys 47
                                                                                                                                                                                                                                                                                                                                                                                                                       16 CCCTGCGTGTGG -----GGTGCTGTGAACTACACTTCCSATTGCAACGGTGAGTGCAAG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hammock, Bruce D.
APPLICANT: Harmock, Bruce D.
APPLICANT: Herrmann, Rafael
APPLICANT: Moskowitz, Haim
TITLE OF INVENTION: Insect Control With Multiple Toxins
NUYBER OF SEQUENCES:
CORRESPONDE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Hsue
STREET: Four Embarcadero Center, Suite 1450
STREET: California
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                            US-09-673-274B-2_CCPY_1_132 (1-132) x US-08-435-040-2 (1-65)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER RELABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATION SYSTEM: PC-50S
SOFTWARE: PATENTIN BATA:
APPLICATION NUMBER: US/09/020,216
FLING APPLICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: US C8/415.040
FLING BATE: 08 MAY-1995
                                                                                                                                                                                                                        Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                          Mismatches:
                                                                                                                                                                                                                                                                                                              Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Siebert, J. Suzanne
REGISTRATION NUMBER: 28,758
REFERENCE/DOCKET NUMBER: 2500.078US0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
US-09-020-216-2
VS-90-more 2, Application US/09020216
Parent No. 6162430
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (415) 362-5556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELERAX: (415) 362-5418
TELEX: 278638 MGPS
INFCRMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                      FRACMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 65 amino acids
TYPE: amino acid
TCPOLOGY: linear
                                                                                                                                                                                                                                            Score: 80.50
Percent Similarity: 57.14%
Best Local Similarity: 40.45%
Outry Match: 30.15%
    : 65 amino acids
amino acid
SY: linear
                                                                  MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .21 TGGTGC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |||||
|:rpCys 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
ZIP: 94111-4121
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                                                                                                                                                                                                      Alignment Scores:
                                                  TOPCLOGY:
                                                                                                               ANTI-SENSE:
                                                                                                                                                          US: 08:435-040-2
    LENGTH:
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                             TYPE:
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5099/D1

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16 TCCTGCGTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGTGAGTGCAAGAGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 SerCysLeuPheGly-----AsnGluGlyCysAsnLysGluCysLysSerTyr 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29 GlyGlySerTyrGlyTyrCysTrpThrTrp---GlyLeuAlaCysTrpCysGlu 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76 GGTTACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGCGAG
                                                                                                                                                                                                                                                                                                                                                                                      JS-09-673-274B-2_COPY_1_132 (1-132) x US-08-682-485A-25 (1-61)
                                                                                                                                                     ORGANISM: Leiurus quinquestriatus quinquestriatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08451472
Patent No. 5770192
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: BIOLOGICAL CONTROL AGENTS
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye PC
STREET: 8th Floor, 1100 No. 5770192th Glebe Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 22201-4714
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,472
                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DAIE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/117,125
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: MARY J WILBON
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 117-187
TELECOMMUNICATION INFORMATION:
TELEFAX: (703) 816 4000
TELEFAX: 200797 NIXM UR
: INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
TENTH: 61 Amino acids
                                                                                                                                                                                                                                                              76.50
55.26%
39.47%
28.65%
                     LENGTH: 61 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l: 61 amino acids
amino acid
SEQUENCE CHARACTERISTICS
                                              LOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTT-SERVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Virginia
': USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Arlington STATE: Virginia
                                                                                                                                                                                                                                                                        Percent Similarity:
West Local Similarity:
Wery Match:
                                                                                                                   ANTI-SENSE: NO
ORIGINAL SOURCE
ORGANISM: Le:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-451-472-4
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                                                                                                                                                                                                                                             red. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 4
                                                                                                                                                                                                                                                                  core:
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Alignment Scores:

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--- -- AsnGluGlyCysAsnLysGluCysLysSerTyr 28
                                                                                                                                                                                               16 TCCTGCGTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGTGAGTGCAAGAGGGG
                                                                                                                                                                                                                                                                                   76 GGTTACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGCGAG 129
                                                                                                                                                                                                                                                                                                        29 GlyGlySerTyrGlyTyrCysTrpThrTrp---GlyLeuAlaCysTrpCysGlu 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: ATKINSON, RCNALD K
APPLICANT: HOWDEN, MERLIN E.H.
APPLICANT: TYLER, MARGARET:
APPLICANT: VONARX, EDWARD 3
ITILE OF INVENTION: Insecticidal Toxins Derived From
ITILE OF INVENTION: Funnel Web (Atrax or Hadronyche Spiders)
                                                                                                                                                    US-09-673-274B-2_COPY_1_132 (1 132) x US-08-451-472-4 (1-61)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leturus quinquestriatus quinquestriatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WEDICK TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS OPTWARE: Patentin Release #1.0, Version #1.25 CURRET APPLICATION DATA: APPLICATION NUMBER: US/08/933,314
                                         Conservative:
Mismatches:
Length:
Matches:
                                                                                    Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: PPD 5099/D1
TELECOMMINICATION INFORMATION:
TELEPHONE: 510-231-1542
TELEFAX: 510-231-1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 17. CULY-1996
APPLICATION NUMBER: US/08/56,933
APPLICATION NUMBER: US/08/256,933
FILING DATE: 27. CULY-1994
APPLICATION NUMBER: WO 93/15:08
FILING DATE: 29. JAN-1993
APPLICATION NUMBER: AU PLC722
FILING DATE: 31. JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 25, Application US/3893314 Patent No. 5959182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Zeneca, Inc.
1200 South 47th Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38,301
                                                                                                                                                                                                                                          13 SerCysLeuPheGly----
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                  76.50
55.26%
39.47%
28.65%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Shaw, Melissa A. REGISTRATION NUMBER: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 61 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zeneca, I
STREET: 1200 South 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
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                           Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94804
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  Pred. No.:
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Sequence 2, Application US/09480251

Sequence 2, Application US/09480251

Patent No. 6465729

GENERAL INFORMATION:
APPLICANT: Defecse, Richard
APPLICANT: Hoffman, Jules
TITLE OF INVENTION: Containing It And Production Of Disease-Resistant
TITLE OF INVENTION: Vector Containing It And Production Of Disease-Resistant
TITLE OF INVENTION: Vector Containing It And Production Of Disease-Resistant
TITLE OF INVENTION: Vector Containing It And Production Of Disease-Resistant
TITLE OF INVENTION: Vector Containing It And Production Of Disease-Resistant
TITLE OF INVENTION: Vector Containing It And Production Of Disease-Resistant
TITLE OF INVENTION: Vector Containing It And Production Of Disease-Resistant
TITLE OF INVENTION: Transpagent Plants
FILE REFERENCE: 2030-01-11
PRIOR APPLICATION NUMBER: BC30-01-11
PRIOR PILING DATE: 1998-07-24
PRIOR PILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 45 
SOFTWARE: FASKEG for Windows Version 3.0
SEQ ID NO 2
LENGTH: 70
LENGTH: 70
TITLE OF INVENTION: Vector Containing It And Production Of Disease-Resistant TITLE OF INVENTION: Transgence Plants
FILE REFERENCE: A32889-FCT-USA-A
CURRENT APPLICATION NUMBER: US/09/480,251
PRIOR APPLICATION NUMBER: PCT/FR98/01462
PRIOR FILING DATE: 1994-07-08
PRIOR FILING DATE: 1997-07-01
PRIOR FILING DATE: 1997-07-01
PRIOR FILING DATE: 1997-07-11
PRIOR FILING DATE: 1997-07-12
PRIOR FILING DATE: 1997-07-12
PRIOR FILING DATE: 1997-07-13
PRIOR FILING DATE: 1997-07-24
NUMBER OF SEC 15 NOS: 15
SOFTHARE: FASTSEQ for Windows Version 3.0
SEQ 1D NO 6
LENGTH: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 ASGAGSSSTTACAAGGSTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGCGAG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 GluGluClyArgSerSerGlyHlSCysSer-----ProSerLeulysCysTrpCysGlu 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 GGTTCCTGC---GTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGTGAGTGCAAG 69
                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: The ubiquitin - drosomycin fusion peptide US-09-480-251-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-C9-673-274B-2_COPY_1_132 (1-132) x US-09-48C-251-6 (1-69)
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
Conservative:
Mismatches:
Indels:
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US-09-480-251-2
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Best Local Similarity:
Query Match:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AsrGluThrCysArgArgValCysLys 24
                                                                                                                                                                                                       TCCTGCGTGTGGGGGTGCTGTGAACTACACTTCCGATTGCAACGGTGAGTGCAAGAGGAGG 75
                                                                                                                                                                                                                                 SGTTACAAGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGCGAG 129
                                                                                                                                                                                                                                                                                                US-09-673-274B-2_COPY_1_132 (1-132) x US-08-933-314-25 (1-61)
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US-09-480-251-6
Sequence 6, Application US/09480251
Parent No. 6465719
GENERAL INFORMATION:
APPLICANT: DeRose, Richard
APPLICANT: Freyssinet, Georges
APPLICANT: Hoffman, Jules
TITLE OF INVENTION: Chimeric Gene Encoding Dicsomyoin,
                        Length:
Matches:
Conservative:
Mismatches:
Indels:
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Indels:
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Matches:
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; ORGANISM: Drosophila melanogaster
US-09-480-251-4
                          0.0418
76.50
55.26$
39.47$
28.65$
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74.50
42.50%
37.50%
27.90%
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Best Local Similarity:
Query Match:
                                                                 Percent Similarity:
Best Local Similarity:
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Pred, No.:
            Alignment Scores
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                                                                                                         Query Match
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Sequence 32120, Application US/09252991A

Sequence 32220, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOWNAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOWNAS

TITLE OF INVENTION: AERUGINOSA FCR D:AGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FCR D:AGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/69/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 3227C
                                                                                                                                                                                                                                                                                                                                                                            45 ArgArgAsnProAsnProPheHisProCys---ProArgAsnCysAlaGlyArgSerAsn 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 TCC-----TCTTGCACTGGTTGC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27 SerArgSerProThrGlyArgTyrThrArgAlaProTrpArgCysCysArgArgArgCys 46
                                                                                                                                                                                                                                                                                                                                     ----TGTAACCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-673-2748-2_COPY_i_132_(1-132) x US-09-252-991A-32270_(1-149)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 AATCGGAAGTGTAGTTCACAGCACCCCACACGCAGGAACCGA 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 CGTTAGCGAAGGAACCGCAGTGACCACCCT ---
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// Parent No. 5770192
// GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32270
0.605
68.00
59.38%
46.88%
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68.00
38.89%
31.48%
28.94%
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Query Match:
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US-08-451-472-6
                                                                                                                                                    Pred. No.:
                                                                                                                                                                        Score:
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Patent No. 6551795
Patent No. 6551795
Patent No. 6551795
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AEROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR PELINGATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                Squence 25, Application US/09403343B
Patent No. 6555091
GENERAL INOFMATION:
APPLICANT: JOLIVET-REYNAUD, COLETTE
APPLICANT: JOLIVET-REYNAUD, COLETTE
APPLICANT: PERRON, HERVE
APPLICANTON POLYPEPTIDE CAPABLE OF REACTING WITH ANTIBODIES OF
TITLE OF INVENTION: POLYPEPTIDE CAPABLE OF REACTING WITH ANTIBODIES OF
TITLE OF INVENTION: POLYPEPTIDE CAPABLE OF REACTING WITH ANTIBODIES OF
TITLE OF INVENTION: POLYPEPTIDE CAPABLE PROPAGA OF TITLE OF INVENTION NUMBER: US/09/403,343B
CURRENT FILING DATE: 1999-10-18
PRIOR PELING DATE: 1997-04-29
PRIOR PELING DATE: 1997-04-29
PRIOR PELING DATE: 1998-04-29
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PATHENT UPF. 2.1
SEQ ID NO 25
LENGTH: 64
                                                                                                                                                                 70 AGGAGGGTTACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGCTGCGAG 129
                                                                                                                                                                                             20 CysAspGlyLeuCysLysasrGlyAlaLysSerGlySerCysGlyPheLeuValPro 39
                                                                                                               GGTTCCTGC---GTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGTGAAG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 TGCAACGGTGAGTGCAAGAGGAGGGTTACAAGGGTGGTCCTTC--
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                                           JS-09-673-274B-2_COPY_1_132 (1-132) x US-09-480-251-2 (1-70)
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Matches:
Conservative:
Mismatches:
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40 SerGlyLeuAlaCysTrpCys 46
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ORGANISM: MSRV
                                                                                                                                                                                                                                                  ESULT 9
IS-09-403-3438-25
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 GlySerTyrGlyTyrCysTrpThrTrp---GlyLeuAlaCysTrpCysGlu 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79 TACAAGGGTGGTCACTGCGGTTCCTTCGCTAACGTGAAUTGCTGCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3. Application US/08435040
Patent No. 5756340
SENERAL INCOMMATION:
APPLICANT: Hermann, Rafael
APPLICANT: Hermann, Rafael
APPLICANT: Moskowitz, Haim
TITLE OF INVENTION: Insect Control With Multiple Toxins
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-673-2745-2_CCPY_1_132 (1-132) x US-08-451-472-6 (1-60)
            TITLE OF INVENTION: BIOLOGICAL CONTROL AGENTS
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSE: Nixon & Vanderhye PC
STREET: 8th Floor, 1100 No. 5770192th Glebe Road
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,472
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Mismatches:
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Four Embarcadero Center, Suite 1450
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
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67.00
56.76%
35.14%
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MOLECULE TYPE: peptide
Us-08-451-472-6
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STATE: California
COUNTRY: U.S.A.
ZIP: 94111-4121
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CITY: Arlington
STATE: Virginia
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Best Local Similarity:
Query Match:
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Fred. No :
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16 TCCTGCGTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGTGAGTGCAAGAGGAGG 75
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APPLICANT: Hermock, Bruce D.
APPLICANT: Hermock, Harm
APPLICANT: Moskowitz, Harm
TITLE OF INVENTION: Insect Control With Multiple Toxins
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSE: Masestic, Parsons, Siebert & Hsue
STREET: Four Embarcadero Center, Suite 1450
CITY: San Francisch
STAREE: California
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PFILING DATE: US/38/435,040
FILING DATE: US-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Siebert, J. Suzanne
REFERENCE/DOCKET NUMBER: 28,758
REFERENCE/DOCKET NUMBER: 28,758
TELEPCOMMUNICATION INFORMATION:
TELEPCOMMUNICATION INFORMATION:
TELEPCOMMUNICATION: 1415; 362-5418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.6, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,216
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Mismatches:
Indels:
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Matches:
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; Sequence 3, Application US/09020216
; Patent No. 6162430
; GENERAL INFORMATION:
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46.15%
33.33%
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 67 aming acids
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TOPOLOGY: linear
MCLECULE TYPE: peptide
HYPOTHETICAL: NO
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ZIP: 94111-4121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CLASSIFICATION:
PRIOR APPLICATION DATA:
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Best Local Similarity:
Query Match:
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16 TCCTGCGTGTGGGGGTGCTGTGAACTACACTTCCGATTGCAACGGTGAGGTGCAAGAGGAGG
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COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE 3.5 INCH
COMPUTER: 18M
OPERATING SYSTEM: MICROSOFT WINDOWS 3.1
SOFTWARE: MICROSOFT WORD FOR WINDOWS 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,383A
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: BA-9063-A
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 80 amino acide
'TYPE: amino acide
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Conservative:
Mismatches:
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Matches:
Conservative:
           FILING DATE: 08-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Stebert, J. Suzanne
REGISTRATION NUMBER: 28,758
REFERENCE/DOCKET NUMBER: 2500.078USO
TELECOMMUNICATION INFORMATION:
TELEFRAX: (415) 362-556
TELEFAX: (415) 362-5418
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 67 amino acids
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APPLICATION NUMBER: US 08/435.040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JS-08-952-383A-14
Sequence 14, Application US/08952383A
Patent No. 6096304
GENERAL INFORMATION:
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64.50
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linear
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                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                              pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
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| Best Local Similarity: 34.21% | M.smatches: 13 | 24.16% | Indels: 2 |
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Command line parameters:

-WODEL=frame+_n2p.model -DEV=x1p

-Q-fcgn2_1/USPTO_spool/US09673274/runat_16102303_176628_2555/app_guery.fasta_1.654

-Q-fcgn2_1/USPTO_spool/US09673274/runat_16102303_176628_2555/app_guery.fasta_1.654

-DB=PIR_76_-OFMT=fastan_-SUPFIX=rpr-MINMATCH=0.1_-LCOPECL=0_-LOOPEXT=0

-UNITS=bits_START=1_-END=-1_-MATRIX=bits_C-TRANS=human40.cdi_-LIGT=45

-COCALIGN=200_-THR_SCORE=pct_-THR_MAX=1C0_-THR_MIN=0_-ALIGN=15_-MODE=LCCAL

-COTFMT=pco_-NORM==xt_-HERPSIXE=500_-MINLEN=0_-MAXIEN=20000000

-USFR=US09673274_@CGN_1 1_77_@runat_16192003_170628_2555_-NOPU=6_-ICPU=3

-NO_MMAP_-LARGEQUERY_-NEG_SCORESO_-WILL -DSPBLOCK=10_-LONGLOG

-DEV_TIMEOUT=120_-WARN_TIMEOUT=30_-THREADS=1_-XGAPOP=:0_-XGAPEXT=0_.5_-FGAPOP=6

-FGAPEXT=7_-YGAPOP=10_-YGAPEXT=6_:5_-DELOP=6_-DELEXT=7_-
                                                                                                                                                                                           October 16, 2003, 17:06:37; Search time 20.7741 Seconds (without allgoments) 1564.690 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                             gataagcttatcggttcctg.....gaacgtgtcgacggatccgg 169
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                               - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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length: 2000000000
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Match Length DB
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Maximum DB seq
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                                                                                                                               OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence:
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76 GGTTACAAGGGTGGTCACTGCGGTTCCTTC----GCTAACGTGAACTGCTGGTGCGAG 129

31 GlyAlaThrSerGlyHisCysGlyPheLeuProGlySerGlyValAlaCysTrpCysAsp

X - scorpion (Leiurus quinquestriatus) Leiurus quinquestriatus hebraeus

neurotoxin C;Species: RESULT 2

drosomycin precurs neurotoxin V-5 - b neurotoxin V - Egy hypothetical prote

D, ò

neurotoxin M14 - 1 neurotoxin 1 - bar neurotoxin IV - Sa

neurotoxin III - s neurotoxin X - sco

Description

crustacean-specifi alpha-toxin Bot XI

neurotoxin III pre neurotoxin IV - Eg

depressant insect

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Ajexperimental source: clone pcD-634
R;Kopeyan, C.; Martinez, G.; Rochat, H.
Eur. J. Blochem. 94, 639-615, 1979
A;Thite: Amino acid sequence of neurotoxin III of the scorpion Androctomus australis H
A;Reference number: A01740; MUID:79148414; PMID:428402
A;Accession: A01740
                                                                                         Tiphartoxin Bot XIV precursor - scorpion (Buthus occitanus)
C;Species: Buthus cocitanus tunetanus
C;Date: 2J-U1-1997 #sequence_revision 01-Aug-1997 #text_change 16-Jul-1999
C;Accession: S68966
E;Accession: S68966
Eur. 2. Biochem: 28, Ducancel, F.; Zencuaki, I.; ben Khalifa, R.; Borchani, L.; Pel
Eur. 2. Biochem: 238, 653-660, 1996
A;Title: A recombinant insect specific alpha-toxin of Buthus occitanus tunetanus scorp
A;Reference number: S68966; MUID:96306228; PMID:8706664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              precu
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A;Residues: 1-84 <BCU>
A;Cross-references: GB:M27703; GB:J05102; NID:g161142; PIDN:AAA29948.1; PID:g161143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ō
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C;Date : 30-Sep:1379 Hesquence_revision 04-Oct-1996 #text_change 18-Jun-1999
C;Accession: C34444; A01746
R;Bougis, P.E.; Rochat, H.; Smith, L.A.
J. Biol. Chem. 264, 19259-19255, 1989
A;Tille: Precursors of Androctohus australis scorpion neurotoxins. Structures
A;Reference number: A34444; MJID:90037662; PMID:2808423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 AsnCysAlaTyrHisCysLeulyslleSerSerGlyCysAspThrLeuCysLysGluAsn 48
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A Status: preliminary
A Molecule type: mRNA
A.Residues: 1-86 ×800>
A.Cross-references: GB:X92376; NID:g1541277; PIDN:CAA63120.1; PID:g1541278
C:Superfamily: Scorption neurotoxin
F;1-148/Domain: signal sequence #status predicted <SIG>
F;19-85/Product: alpha-toxin #status predicted <MIT>
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N,Alternate names: mammalian neurotoxin II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-673-2748-2 (1-169) x S68906 (1-85)
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A;Residues: 20-26,'N',20-83%KOP>
C;Superfamily: scorpton neurotoxin
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                                                                                                                                                                                           and new scorpion
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B) Corso. 0.; Escoubas, P.; Nakajima, T. B. School, Corso. 0.; Escoubas, P.; Nakajima, T. B. School, Corso. 0.; Escoubas, P.; Nakajima, T. B. School, Corso. 0.; Escoubas, P.; Naguence Database, April 2000 School, Corso. O. Corso
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Kyeywords: amidated carboxyl end; neurotoxin; venom
Filb:64,17-37,23,47,27-49/Dissulfide bonds: #status predicted
Fil65/Modified site: amidated carboxyl end (Arg) #status predicted
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48 TrpCys 49
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A,Title: Fuctional duality and structural uniqueness of depressant insect-selective ra, Reference number: A38526, MUID:91230126, PMID:2029523
A,Rocession: B38526
C,Superfamily: scorpion: neurotoxin: venom
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C)Comment: The venom of this scorpion contains three major polypeptide neurotoxins: C.Superfamily: scorpion neurotoxin
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Ryolkova, T.M.; Garsla, A.F.;

Ryolkova, T.M.; Garsla, A.F.;

Bloorg, Khim. 11, 1445:1466, 1985

A;Title: Study of neurotoxins from the venom of central Asian scorpion Buthus of A;Reference number: A94652; MUID: 86110759; PMID: 4091860

A;Accession: JT020

A;Rolecule type: protein

A;Residues: 1-66 ovol.
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C.Species: Mesobuthus eupeus (lesser Asian scorpton)
C.Date: 30-Sep.1988 #sequence_revision 30-Sep-1988 #text_change 31 Dec-1993
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C;Species: Centruroides sculpturatus (bark scorpion)
C;Date: 22-Jun-1981 #sequence_revision 22-Jun-1981 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 CysAspSerGluCysLysLysAsnGlyAlaAspGlySerTyrCysGlnTrpLeuGlyArg
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F::2-65,16-36,22-46,26-48/Disulfide bonds: #status predicted
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R;Babin, D.R.; Watt, D.D.; Goos, S.M.; Mlejnek,
Arch. Biochem. Biophys. 164, 694-706, 1974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 TTCSCTAACGTGAACTGCTGGTGCGAG 129
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ochemistry 30, 4814-4821, 1991
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A;Residues: 1.61 <2LO1>
*Residues: 1.61 <2LO1>
*Residues: 1.62 , 423-426, 1990
A;Title: Primary structure of scorpion anti-insect toxins isolated from the venom of Lei
A;Reference number: $08267; MUID:90184494; PMID:2311768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.Molecule type: protein
A.Residues: 1-65 <KOP>
A.Note: the source is designated as Leiurus quinquestriatus quinquestriatus
C.Reynerfamily: scorpion neurotoxin
C.Reynords: blocked carboxyl end; neurotoxin; sodium channe; inhibitor; venom
F.13-64,17-37,23-47,27-49/Disulfide bonds: #status predicted
F.65/Modified site: blocked carboxyl end (Arg; (probably amidated) #status experimental
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A;Residues: 1-61 <KOP>
R;Zlotkin, E.; Eitan, M.; Bindokas, V.P.; Adams, M.E.; Moyer, M.; Burkhart, W.; Fowler,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Leiurus quinquestriatus (Egyptian scorpion)

C;Apate: 15-Oct-1982 #sequence_revision 27-Nov-1985 #text_change 28-Aug-1998

C;Accession: A01749

R;Kopeyan, C.; Martinez, G.; Rochat, H.

R;Kopeyan, C.; Martinez, G.; Rochat, H.

R;Kopeyan, C.; Martines, G.; Martines,
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                                                                                                                                     SENCYSVALTYIHISCYSVAL-----ProProCysAspGlyLeuCysLysAsn 46
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12 AsnCysValTyrThrCysGlySerAsnSerTyr------CysAsnThrGluCysThr 28
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                                                                                           TCCTGCGTGTGGGGTGCTGTGAACTACACTTCCGATTGCAACGGTGAGTGCAAGAGGAGG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCCTGCGTGTGG-----GGTGCTGTGAACTACACTTCCGATTGCAACGGTGAGTGCAAG 69
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C.Species: Leiurus quinquestriatus quinquestriatus
C.Date: 06-Jul-1990 #sequence revision 06-Jul-1990 #text_change 02-Se
C.Accession: B34123; S0268; B38526
R;Zlotkin, E.; Fowler, E.; Eitan, M.; Moyer, M.; Adams, M.E.
Toxicon 28, 170, 1990
A;Title: On the chemistry and action of the depressant insect toxins.
A;Reference number: A34123
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                            JS-09-673-274B-2 (1-169) x NTSR3A (1-84)
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J. Biol. Chem. 269, 33159-33163, 1994

AyTitle: Insect immunity. Septic injury of Drosophila induces the synthesis of ArReference number: A55824; MUID:95105209; PMID:7806546

ArReference number: A55824; MUID:95105209; PMID:7806546

Arrestalues: 1.70 x FMA

Arross-references: EMBL:X75595; NID:9414661; PIDN:CAA53267.1; PID:9414662

Arross-references: EMBL:X75595; PID:9414661; PID:9414662

Arross-references: EMBL:X75595; PID:9414661; PIDN:CAA53267.1; PID:9414662

Arross-references: EMBL:X75969; PID:9414661; PIDN:CAA53267.1; PID:9414661; PIDN:CAA53267.1; PIDN:CAA53267.1; PID:9414661; PIDN:CAA53267.1; PID:9414661; PIDN
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C;Species: Leiurus quinquestriatus (Egyptian scorpion)
C;Date: 30-Apr-1979 #sequence_revision i3-Jul-1981 #text_change 15-Oct-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         neurotoxin V-5 - bark scorpion
C;Species: Centruroides scuipturatus (bark scorpion)
C;Date: 31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change 07-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 SerCysVal-----AlaAsnAsnTyr------CysAspAsnGlnCysLysMetLys
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7 7 88
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R,David, R.W.; Krishna, N.R.; Watt, D.D.
Toxicon 29, 645-662, 1991
A;Title: Characterization of cationic binding sites of n A;Reference number: A23727; MUID:92021284; PMID:1926166
A;Accession: C23727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
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A/Molecule type: protein
A;Residues: 1-59 <DAC
C)Superfamily: scorpion meurotoxin
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N.Alternate names: cysteine-rich peptide
C.Species: Drosophila melanogaster
C.Saceies: Drosophila melanogaster
C.Data-1995 #sequence_revision C5-Apr-1995 #text_change 21-Jul-2000
C.Accession: A55824, S38575
R.Fenlbaum, P.; Bulet, P.; Michaut, L.; Lagueux, M.; Broekaert, W.F.; Hetru, C.; Hotfman
         Title: Amino acid sequences of neurotoxic protein variants from the venom of Centrurol Reference number: A90058; MUID:75163395; PMID:4460885
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() species: Androccolus australis (Sahara socipion)

() species: Androccolus australis (Sahara socipion)

() cote (Sep-1991 #sequence_revision 10: Sep-1991 #text_change 07-May-1999

() Accession: UC1221

R.Mansuelle, P.; Martin, M.P.; Rochat, H.; Granier, C.

R.Mansuelle, P.; Martin, M.P.; Rochat, H.; Granier, C.

A.Thitle: The amino acid sequence of toxin IV from the Androctonus australis scorpton: A.Reference number: UC121; MJID:94221398; PMIL:1344902

A.Rochession: UC121

A.Mochenie type: protein

A.Residues: 1:64 - MAN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 CysPheTrpLeuGlyLysAsnGluHisAsnThrCysGluCysLysAlaLysAsnGlnGly 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CysTrpCysGlu 49
            A,Title: Amino acid sequences of neurotoxic protein variants A,Reference number: A90058; MUD:75163395; PMID:4460885 A;Accession: A01752 A;Accession: A01752 A;Accession: A01752 A;Accession: A01752 A;Accession: A01752 A;Accession: A)Residues: 1-65 -8AB > C)Superfamily: scorpion neurotoxin C;Reywords: neurotoxin; venom E;127-46,29-48/Disulfide bonds: mstatus predicted
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Cikeywords, neurotoxin
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73 AGGGGTTACAAGGGT ---- GGTCACTGCGGTTCCTTCGCTAACGTGAACTGCTGGTGG 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.3 AsnCysThrCysProGlyLeuGluPheSerAspSerAsnAlaSerCysAsp 349
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Matches:
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A;Introns: 50/2; 84/2; 150/1; 238/3; 342/3; 797/1; 851/1; 947/2; 1017/1; 1083/1
C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
                                                                                                          A;Molecule type: protein
A;Residues: 1-64 <KOP>
C;Superfamily: scorpion neurotoxin
C;Superfamily: scorpion neurotoxin
F;12-63.16-36,22-46,26-48/Disulfide bonds: #status predicted
F;24-63.16-36,22-46,26-48/Disulfide bonds: #status predicted
F;64/Modified site: blocked carboxyl end (Asn) (probably amidated) #status experimental
             R;Kopeyan, C.; Martinez, G.; Rochat, H.
FEBS Lett. 89, 54-58, 1978
A.Title: Amino acid sequence of neurotoxin V from the scorpton Leiurus quinquestriatus
A;Reference number: A0141, MUID:78191225; PMID:658462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Reference number: 220293
A;Accession: TA5972
A;Accession: TA5972
A;Actutus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DnA
A;Residues: 1-1111 < WIL>
A;Cross-references: EMBL:AL032657; PIDN:CAA21739.1; GSPDB:GN00019; CESP:Y47H9C.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   313 ThrGlyLysHisCysAspIleGlyCysSerArgGlyArgPheGlyLeuGlnCysLysGln 332
                                                                                                                                                                                                                                                                                                                                                                                            TGCAACGGTGAGTGCAAGAGGAGGGTTACAAGGGTGGTCACTGC ......GGTTCC 102
                                                                                                                                                                                                                                                                                                                                                                                                              22 CysAs:AspGluCysLysLysLysGlyGlyGlyGlySerGlyTyrCysGlnTrpAlaSerPro 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C;Accession: T26972
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 TTCGCTAACGTGAACTGCTGGTGC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-673-274B-2 (1-169) x NTSR5L (1-64)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: clone Y47H9C
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73.00
60.71$
42.86$
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                                                                           A; Note: L. q. quinquestriatus
A; Accession: A01741
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